

F158-208/Domain: animal Kunitz-type proteinase inhibitor homology <BP>  
F136-86,45-69,61-82,96-149,106-130,122-145,158-208,167-191,183-204/Diulfide bonds: #str

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 3,2e-110;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MDPARLGLSILLPLTEALGDAAPGNNALICLLPLDVGPCALILRYRYDRTQS 60
DB 1 MDPARLGLSILLPLTEALGDAAPGNNALICLLPLDVGPCALILRYRYDRTQS 60
QY 61 CQPLVGGCGGNANNFYTWACDCAWRLEKVPKVCRLQVSDQCEGSTEKTFPFLSSM 120
DB 61 CQPLVGGCGGNANNFYTWACDCAWRLEKVPKVCRLQVSDQCEGSTEKTFPFLSSM 120
QY 121 TCEKPFSGGCHNRIRNRPDPATCMGFCAPKKIPEFCSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKPFSGGCHNRIRNRPDPATCMGFCAPKKIPEFCSPKDEGLCSANVTRYFNPRY 180
QY 181 RCTDAFTYGGCGNDNPFVSRDECKRACAKALKKKKKMPPLAPASRIRIRKKOP 235
DB 181 RCTDAFTYGGCGNDNPFVSRDECKRACAKALKKKKKMPPLAPASRIRIRKKOP 235

```

## RESULT 2

tissue factor pathway inhibitor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #ext\_change 09-Jul-2004

C/Accession: I46937

R.Belaouaj, A.; Kuppunawamy, M.N.; Birktoft, J.J.; Bajaj, S.P.

Thromb. Res. 69, 547-553, 1993

A/Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.

A/Reference number: I46937; MUID:93276427; PMID:8503123

A/Accession: I46937

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-239 <BEL>

A/Cross-references: UNIPROT:PI9761; UNIPARC:UPI000016C6D; GB:861902; NID:9386015; PIND:

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

F149-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>

F120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

F1212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

Query Match 29.9%; Score 390; DB 2; Length 299;

Best Local Similarity 30.8%; Pred. No. 1.1e-27;

Matches 88; Conservative 30; Mismatches 78; Indels 90; Gaps 7;

```

QY 12 LLLPLTEALGDAAPGPTGNN-----BICLLPLDVGPCALLRYRYDRTQ 59
DB 12 LLLPLTEALGDAAPGPTGNN-----BICLLPLDVGPCALLRYRYDRTQ 59
QY 13 LLLGLVPAVSSAAEDFTNITDIKPKPTKSCAMKVDGFCRAIYKXFFPIILTH 72
DB 13 LLLGLVPAVSSAAEDFTNITDIKPKPTKSCAMKVDGFCRAIYKXFFPIILTH 72
QY 60 SCROPVLYGCGEGNANNFYTWACDCAWR-----LEKVPKVCRLQ 99
DB 60 SCROPVLYGCGEGNANNFYTWACDCAWR-----LEKVPKVCRLQ 99
QY 73 QCEEFYGGCGEGNENRPFSLBECCKEACADYPMATTKLTFQKGPFCFLBEPGICR-- 130
DB 73 QCEEFYGGCGEGNENRPFSLBECCKEACADYPMATTKLTFQKGPFCFLBEPGICR-- 130
QY 100 VSDVQCGEGSTEKTFPFLSSMTCSEKPFSGGCHNRIRNRPDPATCMGFC----- 149
DB 100 VSDVQCGEGSTEKTFPFLSSMTCSEKPFSGGCHNRIRNRPDPATCMGFC----- 149
QY 131 -----GYTRFYFNNSKOCERKYGCGCAGL--NNPESLBECCKNTCENTPSDPOVD 180
DB 131 -----GYTRFYFNNSKOCERKYGCGCAGL--NNPESLBECCKNTCENTPSDPOVD 180
QY 150 -----APKKI-----SPFCSPKDEGLCSANVTRYFNPRYRTDAF 186
DB 150 -----APKKI-----SPFCSPKDEGLCSANVTRYFNPRYRTDAF 186
QY 181 DHRITQNTLVNNTLINOPTAPRRMAHGSWCLPDPDRLLCQANERFRFYNAIIGKCRPF 240
DB 181 DHRITQNTLVNNTLINOPTAPRRMAHGSWCLPDPDRLLCQANERFRFYNAIIGKCRPF 240
QY 187 TTTGGGNDNPFVSRDECKRACAKAL-----KXKKKMP 219
DB 187 TTTGGGNDNPFVSRDECKRACAKAL-----KXKKKMP 219
QY 241 KVSQGGGNNENFTSKKACITACKKGRIRNLSKGLIKTRKKKKOP 286
DB 241 KVSQGGGNNENFTSKKACITACKKGRIRNLSKGLIKTRKKKKOP 286

```

## RESULT 3

tissue factor pathway inhibitor precursor (validated) - human

N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #ext\_change 09-Jul-2004

C/Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903

R.Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; Macphail, L.A.; Likert, K.M.; Byers, M.G.;

J. Biol. Chem. 266, 5036-5041, 1991

A/Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro/

A/Reference number: A23712; MUID:91161593; PMID:2002045

A/Accession: A23712

A/Molecule type: DNA

A/Residues: 1-304 <GIR>

A/Cross-references: UNIPROT:PI0646; UNIPARC:UPI0000136C8F; GB:M59493; GB:M59499; NID:9187

Rivan der Logt, C.P.E.; Reitema, P.H.; Bertina, R.M.

Biochemistry 30, 1571-1577, 1991

A/Title: Intron-exon organization of the human gene coding for the lipoprotein-associated

A/Reference number: A39176; MUID:91129227; PMID:1993173

A/Accession: A39176

A/Molecule type: DNA

A/Residues: 1-304 <VAN>

A/Cross-references: UNIPARC:UPI0000136C8F; GB:M58650; GB:J05312; NID:9186827; PIND:AA594

R.Mun, T.C.; Kreitzner, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 263, 6001-6004, 1988

A/Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co

A/Reference number: A28650; MUID:88198127; PMID:2452157

A/Accession: A28650

A/Molecule type: mRNA

A/Residues: 1-304 <MUN>

A/Cross-references: UNIPARC:UPI0000136C8F; GB:J03225; NID:9180545; PIND:AA52022.1; PIND:

A/Note: part of this sequence, including the amino end of the mature protein, was confir

R.Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.J.

Thromb. Res. 55, 37-50, 1989

A/Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated

A/Reference number: A60433; MUID:89388722; PMID:2781520

A/Accession: A60433

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-304 <G12>

A/Cross-references: UNIPARC:UPI0000136C8F

A/Experimental source: endothelial cells

A/Accession: B60433

A/Molecule type: protein

A/Residues: 'XX', 31-53, 'X', 55-56 <G13>

A/Cross-references: UNIPARC:UPI0000173151

A/Experimental source: recombinant material from mouse C137 cells

A/Title: Purification and characterization of the lipoprotein-associated coagulation inh

A/Reference number: A34315; MUID:90036996; PMID:2553722

A/Accession: A34315

A/Molecule type: protein

A/Residues: 'XX', 31-33, 'L', 35-50 <NOV>

A/Cross-references: UNIPARC:UPI0000173152

R.Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.

J. Biol. Chem. 264, 18832-18837, 1989

A/Title: Purification and characterization of the lipoprotein-associated coagulation inh

A/Reference number: A38294; MUID:91009092; PMID:2211593

A/Accession: A38294

A/Molecule type: protein

A/Residues: 29-41 <PED>

A/Cross-references: UNIPARC:UPI0000173154

R.Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.; E

Nature 338, 518-520, 1989

A/Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as

A/Reference number: S03903; MUID:89181950; PMID:2927510

A/Contents: annotation; site-directed mutagenesis

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 19:53:09 ; Search time 40 Seconds  
(without alignments)  
565.273 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPARPLGLSTLLFLTEAA.....KKMPRLRPASRIKIRKQF 235

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

# SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10, 1913

Result No.	Score	Query Match length	DB ID	Description
1	1306	100.0	235	2 A54951
2	390	29.9	299	2 I45937
3	388	29.7	304	1 TIRHGX
4	384.5	29.4	304	1 JC2264
5	376	28.8	302	1 TIRTKX
6	372.5	28.5	300	2 S12143
7	346.5	26.5	396	2 S53325
8	305.5	23.4	2225	2 T26063
9	303	23.2	2167	2 T34395
10	299	22.9	1965	2 T33216
11	292.5	22.4	1558	2 C89114
12	285	21.8	922	2 T23573
13	279.5	21.4	1522	2 H88380
14	271.5	20.8	1416	2 B88550
15	271.5	20.8	2844	2 S28291
16	268	20.5	1474	2 D88550
17	268	20.5	1599	2 T16210
18	253.5	19.4	1043	2 T19734
19	252	19.3	1743	2 T26659
20	240	18.4	1391	2 T20406
21	239	18.3	838	2 T20125
22	235	16.5	252	2 JG0185
23	215	16.5	1208	2 T27822
24	214	16.4	352	1 TIRBOI
25	206	15.8	1303	2 T21275
26	199	15.2	692	2 T32880
27	197	15.1	228	2 T20219
28	196	15.0	123	2 A29652
29	191	14.6	337	1 TIRGBI

## ALIGNMENTS

### RESULT 1

A54951 Tissue factor pathway inhibitor-2 precursor - human

N/Alternate names: placental protein 5 (PP5)

C/Species: Homo sapiens (man)

C/Date: 31-May-1996 #sequence revision 31-May-1996 #text\_change 09-Jul-2004

C/Accession: A54951; I55185; A34029; C34029; B34029

R/Sprecher, C.A.; Kistel, W.; Mathewes, S.; Foster, D.C.

PROG. Nucleic Acids Sci. U.S.A. 91, 3353-3357, 1994

A/Title: Molecular cloning, expression, and partial characterization of a second human c

A/Reference number: A54951; MUID:94211862; PMID:8159751

A/Accession: A54951

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-235 <RES>

A/Cross-references: UNIPROT:P48307; UNIPARC:UPI00000362E2; GB:I27624; NID:9441149; PIDN:J

A/Experimental source: placenta

R/Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Mitsuji, I

J Biochem. 116, 939-942, 1994

A/Title: cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by c

A/Reference number: I55185; MUID:95204397; PMID:7896752

A/Accession: I55185

A/Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI

A/Residues: 1-235 <RES>

A/Cross-references: UNIPARC:UPI00000362E2; GB:I29992; NID:9484050; PIDN:BA06272.1; PID:J

A/Note: parts of this sequence, including the amino end of the mature protein, were deter

R/Buetzow, R.; Huhtala, M.L.; Bohm, H.; Vaitanen, I.; Seppälä, M.

Biochem. Biophys. Res. Commun. 150, 483-490, 1988

A/Title: Purification and characterization of placental protein 5.

A/Reference number: A34029; MUID:88106628; PMID:3276312

hypothetical prote  
alpha-1-microglobu  
alpha-1-microglobu  
alpha-1-microglobu  
gamma-1-microglobu  
alpha-1-microglobu  
hypothetical prote  
hypothetical prote  
venom basic protei  
venom basic protei  
alpha-1-microglobu  
basic proteinase 1  
venom basic protei  
Kunitz-type protei  
basic proteinase 1

hypothetical prote  
alpha-1-microglobu  
alpha-1-microglobu  
alpha-1-microglobu  
gamma-1-microglobu  
alpha-1-microglobu  
hypothetical prote  
hypothetical prote  
venom basic protei  
venom basic protei  
alpha-1-microglobu  
basic proteinase 1  
venom basic protei  
Kunitz-type protei  
basic proteinase 1

C/Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the C/Gene: GDB:127364; OMIM:153310  
 A/Gene: GDB:127364; OMIM:153310  
 A/Cross-references: GDB:127364; OMIM:153310  
 A/Map position: 2q32-2q33  
 A/Introns: 41/1, 107/1, 120/1, 179/1, 210/1, 270/1  
 C/Function:  
 A/Description: regulates clotting by factor Xa-dependent inhibition of the coagulation F  
 A/Pathway: blood coagulation  
 C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>  
 F/54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
 F/284-289/Region: heparin binding #status predicted  
 F/30/Binding site: phosphate (Ser) (covalent) #status experimental  
 F/54-104,63-67,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Dissulfide bonds: #  
 F/64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experim  
 F/135/Inhibitory site: Arg (coagulation factor X) #status experimental  
 F/145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 29.7%; Score 388; DB 1; Length 304;  
 Best Local Similarity 30.3%; Pred. No. 1.7e-27;  
 Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

12 LLLPLTBAALGDAOQ-----PTGNNAEICLLPLDYGCRALLLRYDRT 58  
 17 LLLNLAPAPLADSEDEHTITDTLPLKLMHSFCAPKADGCKAIKMFPI 76  
 QY 59 QSGROPLVGGCEGNANFTWEACDDACR-----IKRKVCRLOVSVDQ-- 105  
 DB 77 RQCEBEPYGGCEBNQKRFESLBECCKKCTRDNNRIITLQCEKDPCLR--BDPGL 133  
 QY 106 CEGSTKYFPNLSSMTCEKPFSGCHNRLENPPDEATCGFC----- 149  
 DB 134 CRGYTRIFNNOTKQCEKPKYGGCLGNM--NNPFTLBCKNTCEGPNQFOVDNYTQL 191  
 QY 150 -----APKCI-----PSPCYSPDEGLCSANVTTRYFNPRTCDAPTYTGG 192  
 DB 192 NAYNNSLTPGSTVPSLPERHGSWCLTPADRGICANENRFFYNVSYGCRPFKSGCG 251  
 QY 193 GNDNFVSRBDCRACAKAL-----KKKKMPKLRPA 224  
 DB 252 GNENFTSKQECRACKKGFQRIKSGGLIKTKRKQKQKXIA 295

RESULT 4  
 JG2264  
 tissue factor pathway inhibitor precursor - rhesus macaque  
 N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi  
 C/Spectra: Macaca mulatta (rhesus macaque)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: JG2264  
 R/Kamel, S.; Kamakubo, Y.; Hamuro, T.; Fujimoto, H.; Ishihara, M.; Yonemura, H.; Miyamoc  
 J. Biochem. 115, 708-714, 1994  
 A/Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path  
 A/Reference number: JG2264; MUID:94375417; PMID:8080987  
 A/Accession: JG2264  
 A/Molecule type: mRNA  
 A/Residues: 1-304 <Rhm>  
 A/Cross-references: UNIPROT:Q28864; UNIPARC:UPI0000136C90; GB:S73337; NID:G665016; PIDN:  
 A/Experimental source: liver  
 C/Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI  
 C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>  
 F/54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

F/54-104,63-67,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Dissulfide bonds: #  
 F/64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted  
 F/135/Inhibitory site: Arg (coagulation factor X) #status predicted  
 F/145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 29.7%; Score 384.5; DB 1; Length 304;  
 Best Local Similarity 30.7%; Pred. No. 3.5e-27;  
 Matches 91; Conservative 37; Mismatches 91; Indels 77; Gaps 10;

1 MDPAPPLGSI-LLLPLTBAALGDAOQ-----PTGNNAEICLLPLDYGCR 46  
 5 MCKVVALWVSIQIMNLAPAPLADSEDEHTITDTLPLKLMHSFCAPKADGCKAIKMFPI 64  
 DB 47 ALLATYYDRYQSGROPLVGGCEGNANFTWEACDDACR-----IKRKVCR 95  
 DB 65 AIKMKFPFPIFTRQCEBEPYGGCEGNANFTWEACDDACR-----IKRKVCR 124  
 QY 96 CRLQVSVDQ--CEGSTKYFPNLSSMTCEKPFSGCHNRLENPPDEATCGFC----- 149  
 DB 125 CPLR--BDPGLCRGYTRIFNNQSKQCEKPKYGGCLGNM--NNPFTLBCKNTCEGL 179  
 QY 150 -----APK--KIPSF-----CSPDEGLCSANVTTRYFNPRT 180  
 DB 180 NGFOVDNYTQLNAYNNSQTPQSTKVPSPFERHGSWCLTPADRGICANENRFFYNVSY 239  
 QY 181 RQCDAPTYTGGCEGNANFTWEACDDACR-----KKKKMPKLRPA 224  
 DB 240 GKCRPFKSGCGENNFYSKRCRACKKGFQRIKSGGLIKTKRKQKQKXIA 295

RESULT 5  
 TIRTK  
 tissue factor pathway inhibitor precursor - rat  
 N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi  
 C/Spectra: Rattus norvegicus (Norway rat)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C/Accession: JX0213  
 R/Injyoti, K.; Eml, M.; Mukai, T.; Kato, H.  
 J. Biochem. 111, 681-687, 1992  
 A/Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).  
 A/Reference number: JX0213; MUID:92348361; PMID:1639767  
 A/Accession: JX0213  
 A/Molecule type: mRNA  
 A/Residues: 1-302 <Rnj>  
 A/Cross-references: UNIPROT:Q02445; UNIPARC:UPI0000136C92; DDBJ:D10926; NID:9220916; PIDN:  
 A/Experimental source: liver  
 C/Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent int  
 C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor  
 C/Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding;  
 F/1-28/Domain: signal sequence #status predicted <SIG>  
 F/29-302/Product: tissue factor pathway inhibitor #status predicted <MAT>  
 F/53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>  
 F/124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>  
 F/222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>  
 F/288-291/Region: heparin binding #status predicted  
 F/53-103,62-66,78-99,124-174,133-157,145-170,222-272,231-255,247-268/Dissulfide bonds: #st  
 F/63/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predict  
 F/134/Inhibitory site: Arg (coagulation factor X) #status predicted  
 F/144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F/222/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 28.8%; Score 376; DB 1; Length 302;  
 Best Local Similarity 33.1%; Pred. No. 2e-26;  
 Matches 84; Conservative 27; Mismatches 76; Indels 67; Gaps 9;

36 CILPLDYGCRALLLRYDRTYQSGROPLVGGCEGNANFTWEACDDAC----- 86  
 DB 53 CMKADGCKAMIRBYTRMNSHOCBRTYGGCRNKRFTLBCKRTCTIPGYKTTI 112  
 QY 87 --WRISKVPKVCRLQVSVDQ--CEGSTKYFPNLSSMTCEKPFSGCHNRLENPPD 141

Db 113 KTTSGARK-PDFCFLB---BDPGICGFMTRFYNNOSKQCEPKYGGCLGN--SNNFET 166  
Qy 142 EATCMGFC-----APKKI-----PSFCYSRK 162  
Db 167 LEECRATCBEPVNEVGKGVYNTQITVTRDTVNNVVIPOATAPAGQMDIDGSCWLCLEPA 226  
Qy 163 DEELCSANTRYRYFNPRYRTCDAPFTTGGCGDNNFVSREDCKRACAK-ALKKKKKMPPL 221  
Db 227 DSELCSASERKFFYNPAIGKRCQFNYTGGCGNNNNFTTKODCNRAKCKOSKSKSSKRAK- 285  
Qy 222 RFASRIKIRKKQ 235  
Db 286 -----TORRRKSF 293

## RESULT 6

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N/Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 16-Jul-1999

C/Accession: S12143; A61373

R/NucleicAcid: R.L.; Girard, T.J.; Broze Jr., G.J.

A/Title: CDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A/Reference number: S12143; MUID:91057146; PMID:2136251

A/Accession: S12143

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-300 &lt;RES&gt;

A/Cross-references: UNIPARC:UPI000016C583; EMBL:X54708; NID:G1612; PIDN:CAJ38515.1; PID:

R/Colburn, P.; Crabdo, J.W.; Buonassisi, V.

J. Cell. Physiol. 148, 320-326, 1991

A/Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell

A/Reference number: A61373; MUID:91349227; PMID:1880157

A/Accession: A61373

A/Molecule type: protein

A/Residues: 25-33, 'X', '35-46 &lt;COL&gt;

A/Cross-references: UNIPARC:UPI0000176246

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C/Keywords: anticoagulant; glycoprotein

F/53-103/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP1&gt;

F/121-171/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP2&gt;

F/113-263/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP3&gt;

Query Match 28.5%; Score 372.5; DB 2; Length 300;

Best Local Similarity 29.7%; Pred. No. 4.2e-26;

Matches 86; Conservative 32; Mismatches 75; Indels 97; Gaps 8;

Qy 12 LILFLTEALGDAAG-----PTGNNAI CLIPLDYGCRAALLRYTD 55  
Db 13 LILGLVPAVSSAAEEDBEFTNTIDIKPLQKPTH8---FCAMKVVDDGFCRAVYIKRFFPN 69  
Qy 56 RYTGSROGLYGGCEGNANFFTWACDCAWR-----IEKVPKY 95  
Db 70 ILAHOCEBPIYGGCEBENRPFSLBCECKKCANADYRMTTKTLTFOKGDPCFLBEPGI 129  
Qy 96 CRLOVSVDDQCSSTKYFPNLSSMTCEKFPSSGCHRRNIEKRPDEATCMGFC----- 149  
Db 130 CR-----GYTRFYNNOSKQCEFKYGGCLGN--NNFSLBCECKKTCENPTSD 177  
Qy 150 -----APKKI-----PSFCYSKDBGLCSANTRYFNPRT 182  
Db 178 FOVDHRTQTLNNTVNTLINQPTAPARRMAFHGVMCLPRAEGLCOANIRFFVYALIGK 237  
Qy 183 CAPFTYGGGNDNNFVSREDCKRACAKL-----KKKKMP 219  
Db 238 GSPFKYSGCGENNETSKKACTACKGPIKSIKGLIKTKRKKKKQ 287

## RESULT 7

S53325

tissue factor pathway inhibitor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-2003  
C/Accession: S53325  
R/Girard, T.J.; Gallant, D.; Broze Jr., G.J.  
Biochem. J. 303, 923-928, 1994  
A/Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals  
A/Reference number: S53325; MUID:95071310; PMID:7980463  
A/Accession: S53325  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-396 <GIR>

A/Cross-references: UNIPARC:UPI0000878B3

C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C/Keywords: serine proteinase inhibitor

F/53-103/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP1&gt;

F/125-175/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP2&gt;

F/309-359/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP3&gt;

Query Match 26.5%; Score 346.5; DB 2; Length 396;

Best Local Similarity 24.6%; Pred. No. 1.2e-23;

Matches 92; Conservative 35; Mismatches 88; Indels 159; Gaps 10;

Qy 12 LILFLTEALG---DAQEPFGNNAI-----CLIPLDYGCRAALLRYTDRTQ 59  
Db 17 LILNCASAPLNAVDBSEBEPGIDBLPPLRLHSFCALKADGFCRAMIRYFNFHTQ 76  
Qy 60 SCROFLYGGCEGNANFFTWACDCAWR-----EKY---PKVCLQVSDQ-- 105  
Db 77 QCEBPIYGGCEGNQNRPFSLBCECKKCVRYKATETLEKLEKPDYCHM---EDSG 133  
Qy 106 CEGSTERTKFPNLSSMTCEKFPSSGCHRRNIEKRPDEATCMGFC----- 149  
Db 134 CNGFTRYNNVNSKCEGFKYGGCLGNL--NNFTLEQCKKTCGSIDLMDETVNTNG 191  
Qy 150 ----- 149  
Db 192 SPGSMNNTSLFNSGSLIPADSGSDMPDSEIGLQHDSESGGLQHDSESG 251  
Qy 150 -----APKKI-----PSFCYS 160  
Db 250 GLQHDSESGGLQHDSESGGLQHDSDNTSPVSVNNDSTPRPPTVYSLFEPYGSWCLT 311  
Qy 161 PDBGLCSANTRYFNPRTCDAPFTTGGCGDNNFVSREDCKRACAKALKKKKKMPK 220  
Db 312 PADRGICHANESRFYNSVIGKCRPFKYSGCGENNETSKKACLTACKGFGHQRISKGG 371  
Qy 221 LRFASRIKIRKKQ 234  
Db 372 L---IKTKRKKKKQ 382

## RESULT 8

T26063

hypothetical protein W01F3.3 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T26063

R/Cummings, P.

submitted to the EMBL Data Library, March 1997

A/Reference number: Z20145

A/Accession: T26063

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-2225 &lt;WIL&gt;

A/Cross-references: UNIPROT:O45881; UNIPARC:UPI00000816RC; EMBL:Z292815; PIDN:CAJ07294.1;

A/Experimental source: clone W01F3

C/Genetics:

A/Gene: CESP:W01F3.3

A/Map position: 5

Query Match 23.4%; Score 305.5; DB 2; Length 2225;

Best Local Similarity 33.7%; Pred. No. 3.1e-19;



	Matches	65;	Conservative	30;	Mismatches	85;	Indels	13;	Gaps	5;
QY	26	OEPTGNNA	MEICLLPLVDYGCRA	LLLRYYDR	TOSCS	CRQFLV	GGCGGN	NNPFTW	EACDA	85
Db	767	EDTTTDS	NNRCLLPHRDS	GNCRGQ	FRWTF	PDDEK	KNCADV	FTTGCC	GNNGNPF	MSKECAAI 826
QY	86	CWRI	EKVPE-----	KVCR	LOVSV	VDQCE	GSGTE	KYKPF	PNLS	SMTC
Db	827	CHKE	PEPTSAT	PTDF	QVCS	NDVDA	-GEC	NGV	YERPA	FADADDCRAFTYGGCGGN--GNN 883
QY	139	PPDE	ATCMGFC--	APK	LP-S	FCYSP	KDQEG	LSAN	VTYR	PRTRTQDAFTYTCCGGND 195
Db	884	FAT	QOECS	RC	CM	MARKKS	PVAT	CEAD	IEV	GCAGVSP
QY	196	NNPVS	RED	CKRAC	208					
Db	944	NNFAT	LG	ECTKNC	956					

```

RESULT 9
T34395
hypothetical protein C37C3.6b - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C|Accession: T34395, T34394
R|Gelsel, C.; Bradshaw, H.,
submitted to The EMBL Data Library, July 1996
A|Description: The sequence of C. elegans coemid C37C3.
A|Reference number: Z21518
A|Accession: T34395
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-2167 <GBI>
A|Cross-references: UNIPROT:O76840, UNIPARC:UPI000007D957, EMBL:U64857, PIDDN:AAC25868.1
A|Experimental source: strain Bristol N2; clone C37C3
A|Accession: T34394
A|Status: preliminary; translated from GB/EMBL/DDBJ
A|Molecule type: DNA
A|Residues: 1-1555, 'SKP', <GB>
A|Cross-references: UNIPARC:UPI0000085C9F, EMBL:U64857, PIDDN:AAC25867.1, GSPDB:GN00023;
C|Genetic:
A|Gene: CBSP:C37C3.6b; CBSP:C37C3.6a
A|Map position: 5
A|Intons: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1, 1556/1
Query Match 23.2%; Score 303; DB 2; Length 2167;
Beat Local similarity 32.3%; Pred. NO.5.1e-19;
Matches 64; Conservative 35; Mismatches 91; Indels 8; Gaps 4;
Cy 29 TGNNAICLLPLDVPCALILRYYYDRYTSRCROFLYGCGCGANNFYTWBACDDACMR 88
Db 1724 TGALPELCMLPEGRSGCYVDNILRMWFDSEKSCQCVTFMTSGCNPNANHTPSQETCERACGX 1783
Cy 89 IEKPYKVCRLQVSVDQCEGSTKEKFPNLSSNTCEKFSSGCGHRRIENRPDEATCMGF 148
Db 1784 WRNV-AVELPAEHGD-QQLAPRWYHDPKTSQCMMMYTGCGGN--GAAPSKKADCSGL 1839
Cy 149 CAPKKIPS----FCVSPDEGLCSANVTTRYYPNPRTCDAFYTYGCGNDNFYSREDC 204
Db 1840 CRVELTNMNNNTDFCTLESAGCPCTDISMWTFDSITLDCKPTTYGGCKGNQNRPFVSKQC 1899
Cy 205 KRAACAKALKKKKKMPKLR 222
Db 1900 QQSRRPGDKTSBEDICTLR 1917
RESULT 10
T33216
hypothetical protein T07H8.4 - Caenorhabditis elegans
C|Species: Caenorhabditis elegans
C|Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C|Accession: T33216

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R.Gattung, S.; Maggi, L.  
submitted to the EMBL Data Library, May 1998  
A.Description: The sequence of C. elegans cosmid T07H8.  
A.Reference number: 221303  
A.Accession: T33216  
A.Status: preliminary; translated from GB/EMBL/DBJ  
A.Molecule type: DNA  
A.Residues: 1-1965 <GAT>  
A.Cross-References: UNIPARC:UPI000017B87E; EMBL:AF067945; PIDDN:AACT7681.1; GSPDB:GN000023;  
A.Experimental source: strain Bristol NZ; clone T07H8  
C.Genetic8:  
A.Gene: CBSP:T07H8.4  
A.Map position: 5  
A.Introns: 47/3; 77/2; 160/3; 198/1; 263/2; 315/1; 386/1; 620/3; 662/1; 706/1; 753/3; 886/1  
Query Match 22.9%; Score 299; DB 2; Length 1965;  
Best Local Similarity 30.0%; Pred. No. 1,1e-18;  
Matches 84; Conservative 24; Mismatches 80; Indels 92; Gaps 12;

QY	31	NNAAI-CLTP--LDYGCRAALL-----RYYDDYTSCHRFVLGGEGGANNFYWEAC	82
Db	1584	NEAFVDCILPMHIGIYGVKNBDSCLPQAGFRFYDDYNTYKCSQMWTYLCGGGANNFYSYEIC	1643
QY	83	DDACCRLEKVPK-----VC-----	96
Db	1644	QRTCSQSP-VPRLEBKRTKRASSFEVCFBPEDRGICGNSSINPIKMTYGNQKTSFTYS	1702
QY	97	-----RLQSVSDPOCE-----GSTEK-----YFNLISMTCKEFP	126
Db	1703	GGCGRRNRFAAQDLCENTCNGCMMNSNDPRICSPSPMGSCNQGLRYWFFYNLTRETCTQFL	1762
QY	127	SGGCHRNRIENRPDEATCMGFCAPKTI PSFCYSPKDEG-LCSANVTTRYTFNPRTYTCDA	185
Db	1763	YGGCGGN--PARRPTLPBICQAKCAVETGTDP-CMESLIRGWSCEMSNRYYFNKRAEOCKG	1819
QY	186	FTYTGCGGNDNNFVSRBDCKRAKAKALKK---KKEMPLR	222
Db	1820	FHYTGCGSGSNNFLTKESCQYCKCEKRPRAAPSKKAKALK	1859

```

RESULT 11
C89I14
protein C37G3_6a [imported] - Caenorhabditis elegans
CISpecies: Caenorhabditis elegans
CIDate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
CAccession: C89I14
RAnonymous: The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A.Reference number: A75000; NUID:99069613; PMID:9851916
A>Note: See webites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
AAccession: C89I14
A>Status: preliminary
AMolecule type: DNA
A.Residues: 1-1558 <STO>
ACross-references: UNIPROT:Q8I710, UNIPARC:UPI0000085C9F, GB:chr_V, PIDN:AAC35867.1; PIR
AGene: C37G3_6a
A.Map position: 5

Query Match          22.4%; Score 292.5; DB 2; Length 1558;
Best Local Similarity 33.0%; Pred. No. 3,2e+18;
Matches      62; Conservative   26; Mismatches    81; Indels     19; Gaps       5;

QY      34 BICLLPDIYGPCRALILRYTYDRYTOSCRDFLYGGCEBGNANNYYTWEACDADCKRIEIKVP 93
        :|::||::|:         ::||:|||||::::|||::|::|::|::|:
DB      1373 DACHINVDGRCKGAEDSWYEIVATGSCTFKXTGGGNNRRPASKDQCBSLC--VRPAS 1430

QY      94 KVCRLGV-----SVDDQ-----CESGTERTFFNLSSWTCSEKFPFGSGCHRNRIENRF 140
        :             ||::|:         |::|::|::|::|::|::|::|::|:
DB      1431 EASASGDIDGAGINSTCDKAQTGPCTNFPTTKKKYNYKPADQTCNRFHVGGOGT--NNRPD 1488
```

QY 141 DEATCMGFCAPKIPSPKDEGLCSAMVTRYENPRRTCDAPFYTGCGGNNFVS 200  
Db 1489 NEQCCRAACQNHK-DACQIPKVOGPGCSGKHSYTYNTASHCETFTYGGCLGNTNRFAT 1546  
QY 201 REDCKRAC 208  
Db 1547 IEECQARC 1554

## RESULT 12

T23573

hypothetical protein K10D3.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C/Accession: T23573

R/Murray, A.  
submitted to the EMBL Data Library, June 1996

A:Reference number: Z19762

A/Accession: T23573

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-922 &lt;MIL&gt;

A/Cross-references: UNIPROT:Q21418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA96886.1;

A/Experimental source: clone K10D3

C/Genetics:

A/Gene: CESP:K10D3.4

A/Map position: 1 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

A/Intons: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 21.8%; Score 285; DB 2; Length 922;

Best Local Similarity 21.9%; Pred. No. 9.2e-18;

Matches 60; Conservative 36; Mismatches 76; Indels 102; Gaps 5;

QY 35 ICLLPDYPCRALLRYYDRYTGSCROFLYGGCGNANFYTWACDCAWRLEKVPK 94  
Db 410 VCKLPREGQNCCTYSNRWFWNATGCEBRTYSGCGNANFETYKCCDYCDNASEPQ 469  
QY 95 -----VCRLOVSVDQC 106  
Db 470 CIOGTALTDNSNGFIICGSSAASSTTCPRANHYTYTGTYGCCPTQATYCSLSYSGASC 529  
QY 107 EGSTERYFNLSMTCEKFPSSGCHNRRIENRPPDEATCMGFCAPKIPSP----- 156  
Db 530 GVAVTWYDSTRTCTQTSFNGCDGN--SNPATQDQDKDVCRAVSCDGDGEVWKEONG 587  
QY 157 -----FCYSPKDEGL-CSA-NVTRY 174  
Db 588 AARACTNRCPSRTHYCTPVTTGTVYQTKSLCPCSKNFVCSQPRDVGVRCSSSTRISRW 647  
QY 175 YFNPRYRTCDAPFYTGCGGNNFVSREDCKRAC 208  
Db 648 YFNADSKTCQTEHYNGCGNRRNFASQKSCQNYC 681

## RESULT 13

H88380

protein T22F7.3 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C/Accession: H88380

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see webites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: H88380

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1522 &lt;STO&gt;

A/Cross-references: UNIPARC:UPI000017ASB5; GB:chr\_III; PIDN:AAA20672.1; PID:G529714; GSF

A/Note: highly similar to ZC84.1

C/Genetics:

A/Gene: T22F7.3  
A/Map position: 3

Query Match 21.4%; Score 279.5; DB 2; Length 1522;

Best Local Similarity 26.0%; Pred. No. 4.7e-17;

Matches 73; Conservative 21; Mismatches 86; Indels 101; Gaps 8;

QY 28 PTGNNAEICLLPDIYPCRALLRYYDRYTGSCROFLYGGCGNANFYTWACDCAW 87  
Db 527 PTAQS--LCTQPRILDCTSAVRWYWNATRSCEWFOYTGCGGNNFVTLMAQCKR 584  
QY 88 RLEKVPK-----VCRLOV 100  
Db 585 GHVEPKCGHGAFRDRNGNFOQSDKQNGPKCPVNVYCSFDGTTGCCPTKAFQCSLNP 644  
QY 101 SYDDQC-EGSTERYFNLSMTCEKFPSSGCHNRRIENRPPDEATCMGFC----- 150  
Db 645 DKGVOGSGRSRYRYNSKQSCSESYQYGCQGN--ANNFVLSDCQHYCGVGCGNGM 702  
QY 151 -----PKIPSP-----FCYSPKDEGL-CSA-N 170  
Db 703 PLRDEATNRMSCSEQKSCPTHECLTIPVNGVSGRCPTQKHICSDPPQGNHSGKIS 762  
QY 171 VTRYENPRYRTCDAPFYTGCGGNNFVSREDCKRACAKA 211  
Db 763 VGRFYNTVTRCATFYNGCNGNINPATQSECNPFCSA 803

## RESULT 14

B88550

protein ZC84.1 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C/Accession: B88550

R/anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A/Reference number: A75000; MUID:99069613; PMID:9851916

A/Note: see webites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg

A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A/Accession: B88550

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1416 &lt;STO&gt;

A/Cross-references: UNIPROT:O03610; UNIPARC:UPI000013BA47; GB:chr\_III; PIDN:CAA79569.1; I

A/Note: similar to Serine protease inhibitor, Kunitz type

C/Genetics:

A/Gene: ZC84.1

A/Map position: 3

Query Match 20.8%; Score 271.5; DB 2; Length 1416;  
Best Local Similarity 24.5%; Pred. No. 2.3e-16;  
Matches 74; Conservative 25; Mismatches 86; Indels 117; Gaps 8;

QY 21 LGDAQEPYGNAR-----ICLLPDIYPCRALLRYYDRYTG 60  
Db 400 IGEBAQR-CQNNAQCPSSHECKADQVCCPRKQTCAQPLRIGDCTENKRYVYARTRQ 458  
QY 61 CROFLYGGCGNANFYTWACDCAWRLEKVPK----- 94  
Db 459 CQMEFYTGCGGNNFVSIMCQNFCKARIEPKICQOAYKDMFGNVTYTGNGKCCPAN 518  
QY 95 -----VCRLOVSVDQC-EGSTERYFNLSMTCEKFPSSGCHNRRI 135  
Db 519 YECYFDGSGQCCPTKAFQCSLNDSDGIQCGAGSFFKXYNPQTONGCSFOYNGCDGN-- 576  
QY 136 ENRPDEATCMGFCAPKIPSP----- 156  
Db 577 SNNFANRDACSYGSGVGGCPGGLPLRDHSGWVWGAQOTSQPSHSCIPVLVGNLSLN 636  
QY 157 -----FCYSPKDEGL-CSAN-VTRYENPRYRTCDAPFYTGCGGNNFVSREDCKR 206  
Db 637 RCCEPRAYMGLPFGQGTGCGANFYVGRYFYIVTSQCTSPFGGCGGNNFVLIQCCAN 696

Qy 207 AC 208  
DB 697 FC 698

## RESULT 15

828291  
hypothetical protein ZC84.1 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C/Accession: 828291

R/Thomas, K.

Submitted to the EMBL Data Library, December 1992

A/Reference number: 828285

A/Accession: 828291

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-2844 &lt;THO&gt;

A/Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCB9; EMBL:Z19157

C/Genetic: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12

493/1; 2555/1; 2720/1; 2739/3; 2819/1

F/1220-274/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP11&gt;

F/143-395/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP12&gt;

F/142-492/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP13&gt;

F/146-598/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP14&gt;

F/154-706/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP15&gt;

F/1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP16&gt;

F/1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP17&gt;

F/1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP18&gt;

F/1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP19&gt;

F/2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology &lt;BP10&gt;

Query Match 20.8%; Score 271.5; DB 2; Length 2844;

Best local similarity 24.5%; Pred. No. 4.5e-16;

Matches 74; Conservative 25; Mismatches 86; Indels 117; Gaps 8;

Qy 21 LGDAQEPFGNNAE-----ICLLPLDYGPCRALILRYTYDRYTOS 60  
DB 408 IGBEAQR-CQNNACPSHSECKADQGVCCPRKOTICAPLRIGDCTENVKRYNNATRQ 466  
Qy 61 CRQFLYGGCGGNANFTWAEACDCAWRIRKPK----- 94  
DB 467 CQMFETYGCGGNDFDSIMDCQNFCKNAIPBPKCIQQAAYKDMFGNFTCSNGMCCPAN 526  
Qy 95 -----VCRLQVSVDDQC-EGSTEKYPFNLSMTCEKFPFGGCHRRRI 135  
DB 527 YECYFDGSGWCCPTKAFPTSLNTDSTIGCGAGSTFKYYINPQTQNCESFOYNGCDGN-- 584  
Qy 136 ENRPDEATCMGFCAPKRIPS----- 156  
DB 585 SNNFANRDACESYCVGCGFNGGTPLRDHSGMVMVCAQQTSCPDHSECIPLVGNGLIN 644  
Qy 157 -----PCYSPDEGL-CSAN-VTRYYNPRYRTCDATYTGCGGDNPPVSRBEDCKR 206  
DB 645 RCCEPTRAVMGCLPQGGTQCGANVYRYYNIVTSQCTSPFGCGDGNANFLNIQCCRN 704  
Qy 207 AC 208  
DB 705 FC 706

Search completed: March 9, 2006, 19:57:33  
Job time: 42 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 19:49:49 ; Search time 230 Seconds

(without alignments)  
720.866 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPARPLGSLILPLTEAA.....KMPKLRFPASIRIKRKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1306	100.0	235	1	TPPI2_HUMAN	P48307 homo sapien
2	1306	100.0	235	2	06ME6_HUMAN	06ME6 homo sapien
3	1231.5	94.3	224	2	08NAK6_HUMAN	08NAK6 homo sapien
4	94.3	72.2	167	2	08NE89_HUMAN	08NE89 homo sapien
5	939.5	71.9	234	2	07YRQ8_BOVIN	07YRQ8 bos taurus
6	654	50.1	230	2	08CF99_RAT	08CF99 ratius norv
7	644	49.3	230	1	TPPI2_MOUSE	035536 mus musculu
8	635	48.6	224	2	07T0Z5_XENLA	07T0Z5 xenopus lae
9	630	48.2	219	2	05FYV6_XENTR	05FYV6 xenopus tro
10	458	35.1	190	2	04RDL7_TETNG	04RDL7 tetraodon n
11	396	30.3	304	2	05RFP8_PONPY	05RFP8 pongo pygma
12	388	29.7	304	1	TPPI1_HUMAN	P10646 homo sapien
13	388	29.7	304	2	05JTS4_HUMAN	05JTS4 homo sapien
14	387.5	29.7	300	1	TPPI1_FABIT	P19761 cryctolagus
15	387	29.6	287	2	093424_CYPCA	093424 cyprinus ca
16	384.5	29.4	304	1	TPPI1_MACMU	028864 macaca mula
17	378	28.9	306	1	TPPI1_MOUSE	054819 mus musculu
18	376	28.8	302	1	TPPI1_RAT	002445 ratius norv
19	367.5	28.1	279	2	07Z242_BRABR	07Z242 brachydanto
20	367.5	28.1	292	2	0504K2_BRABR	0504K2 brachydanto
21	361	27.6	2419	2	07FXZ1_ANOCA	07FXZ1 anopheles g
22	358.5	27.5	759	2	08IT91_AMCSA	08IT91 ancylostoma
23	357.5	27.4	3198	2	09UG88_MANSB	09UG88 manduca sex
24	346.5	26.5	396	2	028874_CANPA	028874 canis famli
25	336.5	25.8	2772	2	09VAV4_DROME	09VAV4 drosoophila
26	336.5	25.8	2776	2	0869A0_DROME	0869A0 drosoophila
27	336.5	25.8	2894	2	07KXK2_DROME	07KXK2 drosoophila
28	336.5	25.8	2898	2	086829_DROME	086829 drosoophila
29	331.5	25.4	419	2	04SB60_TETNG	04SB60 tetraodon n
30	325	24.9	1572	2	044938_HAECC	044938 haemochus
31	310.5	23.8	2163	2	061TS1_CAEBR	061TS1 caenorhabd1

32	310.5	23.8	2174	2	09G0R0_DROME	09G0R0 drosoophila
33	305.5	23.4	2225	2	045881_CAEBR1	045881 caenorhabd1
34	305	23.4	1487	2	08MPV5_CAEBL	08MPV5 caenorhabd1
35	303	23.2	2167	2	076840_CAEBL	076840 caenorhabd1
36	301	23.0	2157	2	060797_CAEBR	060797 caenorhabd1
37	300	23.0	1604	2	05ZK35_CAEBL	05ZK35 caenorhabd1
38	300	23.0	1818	2	05ZK36_CAEBL	05ZK36 caenorhabd1
39	300	23.0	1954	2	05ZK37_CAEBL	05ZK37 caenorhabd1
40	300	23.0	1995	2	05ZK39_CAEBL	05ZK39 caenorhabd1
41	300	23.0	2006	2	05ZK40_CAEBL	05ZK40 caenorhabd1
42	300	23.0	2007	2	05ZK42_CAEBL	05ZK42 caenorhabd1
43	295.5	22.6	1979	2	060WPI_CAEBR	060WPI caenorhabd1
44	292.5	22.4	1558	2	081710_CAEBL	081710 caenorhabd1
45	285	21.8	568	2	060Q68_CAEBR	060Q68 caenorhabd1

#### ALIGNMENTS

RESULT 1  
ID TPPI2\_HUMAN STANDARD; PRT; 235 AA.  
AC P48307;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE tissue factor pathway inhibitor 2 precursor (TPPI-2) (placental protein 5) (Pp5).  
GN Name=TPPI2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.  
NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=95204397; PubMed=7896752;  
RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F., Aoki I., Misugi K., Umeda M., Miyazaki K.;  
RT "cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by cancer cells: identification as placental protein 5 and tissue factor pathway inhibitor-2.";  
RT J. Biochem. 116:939-942(1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Placenta;  
RX MEDLINE=94211862; PubMed=8159751;  
RA Sprecher C.A., Kistiel W., Mathewes S., Foster D.C.;  
RT "Molecular cloning, expression, and partial characterization of a second human tissue-factor-pathway inhibitor.";  
RT Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Maggi L.;  
RT Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=12477932; PubMed=11342222; DOI=10.1016/S0167-4781(00)00298-0;  
RA Kamei S., Kazama Y., Kujiiper J.L., Foster D.C., Kistiel W.;  
RT "Genomic structure and promoter activity of the human tissue factor pathway inhibitor-2 gene.";  
RT Biochim. Biophys. Acta 1517:430-435(2001).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Krausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Schemm C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitley M., Madan A., Young A.C., Snevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smolins D.E.,  
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN  
RN PARTIAL PROTEIN SEQUENCE OF 23-35; 47-53 AND 133-146.  
RP TISSUE=Placenta;  
RX MEDLINE=88106628; PubMed=3276312;  
RA Buertow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;  
RT "Purification and characterization of placental protein 5.";  
RL Biochem. Biophys. Res. Commun. 150:483-490(1988).  
RN  
RN ERRATUM.  
RA Buertow R., Huhtala M.-L., Bohn H., Virtanen I., Seppaelae M.;  
RL Biochem. Biophys. Res. Commun. 151:630-631(1988).  
CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,  
CC weakly factor Xa. Has no effect on thrombin.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,  
CC placenta, heart, pancreas, and maternal serum at advanced  
CC pregnancy.  
CC -1- DOMAIN: This inhibitor contains three inhibitory domains.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC -----  
CC EMBL; D29992; BAA06272.1; -; mRNA.  
CC EMBL; L27624; AAA0094.1; -; mRNA.  
CC EMBL; AC002076; AAS02022.1; -; Genomic DNA.  
CC EMBL; AF217542; AK13254.1; -; Genomic DNA.  
CC EMBL; BC005330; AA05330.1; -; mRNA.  
CC PIR; A54951; A54951.  
CC HSSP; P10646; 1IRH.  
CC DR Ensembl; ENSG0000105825; Homo sapiens.  
CC DR HGNC; HGNC:11761; TPPI2.  
CC DR H-InvDB; HIX006849; -.  
CC DR MIM; 600033; -.  
CC DR GO; GO:0005578; Extracellular matrix (sensu Metazoa); TAS.  
CC DR GO; GO:0005201; Extracellular matrix structural constituent; TAS.  
CC DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
CC DR InterPro; IPR008296; Prot\_inh\_TPPI.  
CC DR Pfam; PF00014; Kunitz\_BPTI; 3.  
CC DR PIRSF; PIRSF01620; TPPI\_1.  
CC DR PRINTS; PR00759; BASICTPASE.  
CC DR PRODOM; PD000222; Prot\_inh\_Kunz-m; 3.  
CC DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
CC DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
CC DR Blood coagulation; Direct protein sequencing; Glycoprotein;  
CC KM Polymorphism; Protease inhibitor; Repeat; Serine protease inhibitor;  
CC KW signal.  
CC FT SIGNAL. 1 22  
CC FT CHAIN 23 235 Tissue factor pathway inhibitor 2.  
CC FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.  
CC FT DOMAIN 96 149 BPTI/Kunitz inhibitor 2.  
CC FT DOMAIN 158 208 BPTI/Kunitz inhibitor 3.  
CC FT COMBINS 213 217 Poly-Iys.  
CC FT SITE 46 47 Reactive bond (By similarity).  
CC FT SITE 107 108 Reactive bond (By similarity).  
CC FT SITE 168 169 Reactive bond (By similarity).

FT CARBOHYD 116 116 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 116 170 N-linked (GlcNAc...) (Potential).  
FT DISULFID 370 86 By similarity.  
FT DISULFID 45 69 By similarity.  
FT DISULFID 61 82 By similarity.  
FT DISULFID 96 149 By similarity.  
FT DISULFID 106 130 By similarity.  
FT DISULFID 122 145 By similarity.  
FT DISULFID 158 208 By similarity.  
FT DISULFID 167 191 By similarity.  
FT DISULFID 183 204 By similarity.  
FT VARIANT 102 102 V->A (in dbSNP:1804202).  
FT  
FT CONFLICT 23 23 /FTID=VAR\_012005.  
FT SQ SEQUENCE 235 AA; 26934 MW; 975ABA5C53F7C65F CRC64;  
SQ  
Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4e-11;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 61 CRQPLYGCGEYANNFYTWACDDACWRIEKYPRYCRLOVSYDDCGESTERYFNLSSM 120  
DB 61 CRQPLYGCGEYANNFYTWACDDACWRIEKYPRYCRLOVSYDDCGESTERYFNLSSM 120  
QY 121 TCEKFFSGGCHNRLENRPEPDATCGPCAPKRTSPCSPDEGLCSANVRYRNPY 180  
DB 121 TCEKFFSGGCHNRLENRPEPDATCGPCAPKRTSPCSPDEGLCSANVRYRNPY 180  
QY 181 RTCDAPFYTGCGANNFYVRDCRACAKALKKKKKPKLPASRIRKIKQF 235  
DB 181 RTCDAPFYTGCGANNFYVRDCRACAKALKKKKKPKLPASRIRKIKQF 235  
QY 181 RTCDAPFYTGCGANNFYVRDCRACAKALKKKKKPKLPASRIRKIKQF 235  
DB 181 RTCDAPFYTGCGANNFYVRDCRACAKALKKKKKPKLPASRIRKIKQF 235  
RESULT 2  
Q66M88 HUMAN PRELIMINARY; PRT; 235 AA.  
AC 066M88;  
ID 25-OCT-2004 (TREMblrel. 28, Created)  
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)  
DE Tissue factor pathway inhibitor 2.  
GN Name=TPPI2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
OX  
RN NUCLEOTIDE SEQUENCE.  
RA Xu Y., Li T., Du G.;  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC EMBL; AY691946; AAU04568.1; -; mRNA.  
CC DR GO; GO:0005576; Extracellular region; IEA.  
CC DR GO; GO:0030414; Protease inhibitor activity; IEA.  
CC DR GO; GO:0004867; Fibrinogen-type endopeptidase inhibitor activity; IEA.  
CC DR GO; GO:0007596; Fibrinogen-type endopeptidase inhibitor activity; IEA.  
SQ SEQUENCE 235 AA; 26934 MW; 975ABA5C53F7C65F CRC64;  
SQ  
Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 5.4e-11;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
DB 1 MDPAPPLGISILLFLTEALGDAAQEPYNNALICLLPLDYGPCRALILRYRDRYTS 60  
QY 61 CRQPLYGCGEYANNFYTWACDDACWRIEKYPRYCRLOVSYDDCGESTERYFNLSSM 120  
DB 61 CRQPLYGCGEYANNFYTWACDDACWRIEKYPRYCRLOVSYDDCGESTERYFNLSSM 120



DB 61 CROFLYGCGCGNANNFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKCYFNNLSM 120  
 QY 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRY 180  
 DB 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRY 180  
 QY 181 RTCDATFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 235  
 DB 181 RTCDATFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 235

RESULT 3  
 Q8NAK6\_HUMAN  
 ID Q8NAK6\_HUMAN PRELIMINARY; PRT; 224 AA.  
 AC Q8NAK6;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ35180.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 PubMed=14702039; DOI=10.1038/ng1285;  
 Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Matita H.,  
 Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 Yamamoto J.-I., Saito K., Kawai I., Isono Y., Nakamura Y., Nagatsuma M.,  
 Shiratori A., Sudo H., Hoshiro T., Kaku Y., Kodaira H., Komodo H.,  
 Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K.,  
 Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
 Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,  
 Ishida S., Oho Y., Takiguchi S., Watanabe S., Yoshida T., Hotsuta T.,  
 Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
 Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,  
 Iinoe N., Masehino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,  
 Yoshihawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
 Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujisawa T.,  
 Oono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,  
 Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 Nakai K., Iada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
 RT Complete sequencing and characterization of 21,443 full-length human  
 cDNAs.";  
 RL Nat. Genet. 36:40-45(2004).  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL; AK092499; BAC03906.1; -; mRNA.  
 DR HSP; P10646; IIRH.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.  
 DR GO; GO:000467; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro; IPR008296; Prot\_inh\_TPTI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PIRSF001620; TPTI; 1.  
 DR PRINTS; PIRSF00759; BASICPTASB.  
 DR PRODOM; PD000223; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR SMART; SM00131; KU; 3.

DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 224 AA; 25795 MW; F586328C3144765 CRC64;  
 Query Match 94.3%; Score 1231.5; DB 2; Length 224;  
 Best Local Similarity 95.3%; Pred. No. 3.3e-104;  
 Matches 224; Conservative 0; Mismatches 0; Indels 11; Gaps 1;  
 QY 1 MDPARPLGLSILLFLTEALGDAAPFTGNNAEICLPDVPCCALLIRYYDRYTOS 60  
 DB 1 MDPARPLGLSILLFLTEALGDAAPFTGNNAEICLPDVPCCALLIRYYDRYTOS 49  
 QY 61 CROFLYGCGCGNANNFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKCYFNNLSM 120  
 DB 50 CROFLYGCGCGNANNFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKCYFNNLSM 109  
 QY 121 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRY 180  
 DB 110 TCCKPFGGCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRY 169  
 QY 181 RTCDATFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 235  
 DB 170 RTCDATFTYTCGGGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 224

RESULT 4  
 Q8NEB9\_HUMAN  
 ID Q8NEB9\_HUMAN PRELIMINARY; PRT; 167 AA.  
 AC Q8NEB9;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Similar to tissue factor pathway inhibitor 2 (Fragment).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Placenta;  
 RC Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.  
 DR EMBL; BC034155; AA034155.1; -; mRNA.  
 DR HSP; P10646; IIRH.  
 DR GO; GO:000467; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PRINTS; PR00759; BASICPTASB.  
 DR PRODOM; PD000223; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 2.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 1.  
 DR PROSITE; PS50279; BPTI\_KUNITZ\_2; 2.  
 FT NON TER 1  
 SQ SEQUENCE 167 AA; 19365 MW; 16C204B96071F27D CRC64;  
 Query Match 72.2%; Score 943; DB 2; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-78;  
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 69 CEGNANNFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKCYFNNLSMTCCKPFG 128  
 DB 1 CEGNANNFYTWACDCAWRIKVPKVCRLQVSVDDQCGSGSTKCYFNNLSMTCCKPFG 60  
 QY 129 GCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRYRTCDATFTY 188  
 DB 61 GCHRRRIENRFPDEATCMGFCAPKIPSCYSPKDEGLCSANVTYYFNPRYRTCDATFTY 120  
 QY 189 TGGCGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 235  
 DB 121 TGGCGNDNNFVSRBDCRCACAKALKKKKMPRLRPSASRIKIRKQF 167

```

RESULT 5
Q7YR08 BOVIN
ID Q7YR08 BOVIN PRELIMINARY; PRT; 234 AA.
AC Q7YR08
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2802738; Pubmed=12921785; DOI=10.1016/S0003-9661(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kistiel W.,
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2."
Arch. Biochem. Biophys. 417:96-104(2003).
[2]
RN
RP NUCLEOTIDE SEQUENCE.
RA Deng F.-M., Kistiel W., Sun T.-T.,
RT Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; A084035.1; -; mRNA.
DR HSSP; P00981; 1DTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008296; Prot_inh_TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PIRSF; PIRSF01620; TFPI. 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401BEC84D589B422 CRC64;

Query Match 71.9%; Score 939.5; DB 2; Length 234;
Best Local Similarity 72.2%; Pred. No. 1.5e-77;
Matches 171; Conservative 23; Mismatches 38; Indels 5; Gaps 3;

QY 1 MDPARPLGISILLFLTEALGDAAQEPGNNAEICLLPLDYGPCRALLRYYDRTYQS 60
DB 1 MDSVRLPLMLLSLLLVGTALGASQAPPGNNAEICLLPPDGPCCARIRPSYYDRTYQS 60
QY 61 CROFLVGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTEKYFFNLSM 120
DB 61 CREFTVGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTEKYFFNLSM 119
QY 121 TCSEKPSGGCHNRRIENRPDEATCMGFCAPKXI-PSFCYSPKDEGLCSANVTYYFNPR 180
DB 120 TCCKFTISGGCHSN--ENRPDEATCMDFCAPKRAPVFCYSPKDEGLCSANVTYYFNPR 177
QY 181 RTGDAFTYGGCGGNDNNPVRBEDCKRACAKLKKK--KKPKRFPASRIKRIKKQF 235
DB 178 KACEAFNRYTGCGGNDNNPVALKDKCKTCVAKLKKKKKPKRILLANRLRIKKQF 234

RESULT 6
Q8CF99 RAT
ID Q8CF99 RAT PRELIMINARY; PRT; 230 AA.
AC Q8CF99
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2 precursor.
GN Name=cfpi-2;

```

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley; TISSUE=Placenta;
RX MEDLINE=22183372; Pubmed=12195712;
RA Hiseaka T., Kistiel W., Rosenbaum J.;
RT "cDNA cloning and tissue distribution of the rat ortholog of tissue
factor pathway inhibitor-2."
Thromb. Haemost. 88:356-357(2002).
RL
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AJ428954; CAD22046.1; -; mRNA.
DR HSSP; P10646; 1IRH.
DR Ensemble; ENSRNOG0000010513; Rattus norvegicus.
DR RCD; 628629; TFPI2.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0030414; F:protease inhibitor activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008296; Prot_inh_TFPI.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR PIRSF; PIRSF01620; TFPI. 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
DR Signal.
FT CHAIN 1 25
FT SIGNAL 25 230
SQ SEQUENCE 230 AA; 26157 MW; 07CCD5B9F7D43BD9 CRC64;

Query Match 50.1%; Score 654; DB 2; Length 230;
Best Local Similarity 55.6%; Pred. No. 1.7e-51;
Matches 129; Conservative 25; Mismatches 74; Indels 4; Gaps 3;

QY 1 MDPARPLGISILLFLTEALGDAAQEPGNNAEICLLPLDYGPCRALLRYYDRTYQS 60
DB 1 MDPATSLRLMNLPLLVGSLGASVSAQGNNAEICLLPLDYGPCRALLRYYDRTYQS 60
QY 61 CROFLVGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTEKYFFNLSM 120
DB 61 CREFTVGGCEGNANFYTWACDCAWRIRKVPVCHLQVSVDDCGEGSTEKYFFNLSM 119
QY 121 TCSEKPSGGCHNRRIENRPDEATCMGFCAPKXI-PSFCYSPKDEGLCSANVTYYFNPR 179
DB 120 TCSEPLRPLGLC--SRITNVPPPEAMCKSLCEPRKSI-PSFCSPKDEGLCSANVTYYFNPR 177
QY 180 YRTGDAFTYGGCGGNDNNPVRBEDCKRACAKLKKKKKPKRFPASRIKRIK 231
DB 178 NRTCEFTYTGCGGNDNNFYLDACNRACVAKLKKRKRRIKIDFPLRPMKLR 229

RESULT 7
TFPI2 MOUSE
ID TFPI2 MOUSE STANDARD; PRT; 230 AA.
AC Q35356
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tissue factor pathway inhibitor 2 precursor (TFPI-2).
GN Name=TFPI2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN-1CR: TISSUB=Placenta;  
 RX MEDLINE=97101108; PubMed=8945635;  
 RA Miyagi Y., Yasumitsu H., Mizushima H., Koshikawa N., Matsuda Y.,  
 RA Itoh H., Hori T., Aoki T., Mitsuji K., Miyazaki K.;  
 RT Cloning of the cDNA encoding mouse pps/TPPI-2 and mapping of the gene  
 RT to chromosome 6.";  
 RL Tissue Cell Biol. 15:947-954(1996).  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/SvJ;  
 RX MEDLINE=20132652; PubMed=10669168;  
 RA Kazama Y., Kamel S., Kuyper J.L., Foster D.C., Kistiel W.;  
 RT "Nucleotide sequence of the gene encoding murine tissue factor pathway  
 RT inhibitor-2.";  
 RL Thromb. Haemost. 83:141-147(2000).  
 RN  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tothlyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schenker A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,  
 CC weakly factor Xa. Has no effect on thrombin.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta. Also expressed  
 CC in liver and kidney.  
 CC -1- DOMAIN: This inhibitor contains three inhibitory domains.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL: D50586; BAA22585.1; -; mRNA.  
 DR EMBL: AF180353; AAP40412.1; -; Genomic DNA.  
 DR EMBL: BC021639; AAP21639.1; -; mRNA.  
 DR HSPB: P10646; IIRH.  
 DR Ensembl: ENSMUSG00000029664; Mus musculus.  
 DR MGI: MGI:108543; Tfp12.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR InterPro: IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro: IPR008296; Prot\_inh\_TfPI.  
 DR Pfam: PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF: PIRSF001620; TFPI; 1.  
 DR PRINTS: PR00759; BASICTPASE.  
 DR PRODOM: PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART: SMO0131; KU; 3.  
 DR PROSITE: PS00280; BPTI\_KUNITZ\_1; 2.  
 DR PROSITE: PS00279; BPTI\_KUNITZ\_2; 3.  
 KW Blood coagulation, glycoprotein, Protease inhibitor, Repeat,  
 KW Serine protease inhibitor, Signal.  
 FT SIGNAL 1 22 By similarity.  
 FT CHAIN 23 230 Tissue factor pathway inhibitor 2.

FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.  
 FT DOMAIN 96 146 BPTI/Kunitz inhibitor 2.  
 FT DOMAIN 156 206 BPTI/Kunitz inhibitor 3.  
 FT SITE 46 47 Reactive bond (by similarity).  
 FT SITE 106 107 Reactive bond (by similarity).  
 FT SITE 166 167 Reactive bond (by similarity).  
 FT CARBOHYD 168 168 N-linked (GlcNAc...) (potential).  
 FT CARBOHYD 178 178 N-linked (GlcNAc...) (potential).  
 FT DISULFID 36 86 By similarity.  
 FT DISULFID 45 69 By similarity.  
 FT DISULFID 61 82 By similarity.  
 FT DISULFID 96 146 By similarity.  
 FT DISULFID 105 129 By similarity.  
 FT DISULFID 121 142 By similarity.  
 FT DISULFID 156 206 By similarity.  
 FT DISULFID 165 189 By similarity.  
 FT DISULFID 181 202 By similarity.  
 FT DISULFID 230 AA; 26137 MW; 57EADB2B36521C7B CRC64;  
 SQ SEQUENCE  
 Query Match 49.3%; Score 644; DB 1; Length 230;  
 Best Local Similarity 56.4%; Pred. No. 1,4e-50;  
 Matches 123; Conservative 26; Mismatches 65; Indels 4; Gaps 3;  
 QY 1 MDPARPLGSLILLFLTEALGDAOEPYNNALCLLPDYPCRALIRYTDYTGQ 60  
 DB 1 MDPAMPPLQMLNPLLVGLVSVAGNNLEICLPADAPQCALIPKPYDRDQOK 60  
 QY 61 CRQFLYGGCGANNPTTWEACDADCKRIKRYKRYCRLQVSDQCGSTREKYPENLSSM 120  
 DB 61 CRFPYGGCGANNPTTWEACDADCKRIKRYKRYCRLQVSDQCGSTREKYPENLSSM 119  
 QY 121 TCERFSGGCHRRIRNRPDPBATCMGFCAPK-IPSCYSPKDEGLCSANVTREYENPR 179  
 DB 120 TCERPLRGGLC-SRTIVSEBETKGLCEPRKHIPFSCSPDDEGLCSANVTREYENPR 177  
 QY 180 YRTCDATYTCGGNDNPFVSRDCKRCAKALKKKK 217  
 DB 178 NKCEFTTYTGGCGNNPFYLLDACHRACVKGMKKPR 215  
 RESULT 8  
 ID 077025 XENLA PRELIMINARY; PRT; 224 AA.  
 AC 077025;  
 DT 01-OCT-2003 (TREMblrel. 25, Created)  
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 25, Last annotation update)  
 DE MG68843 protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodinae; Xenopus; Xenopus.  
 CC NCBI\_TaxID=8355;  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tothlyuk S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2].  
 RN NCUTEOTIDE SEQUENCE.  
 RP TISSUE=Embryo;  
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative";  
 RT Dev. Dyn. 225:384-391(2002).  
 RL [3].  
 RN NCUTEOTIDE SEQUENCE.  
 RP TISSUE=Embryo;  
 RC Klein S., Strausberg R.,  
 RA Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL; BC055972; AAH55972.1; -; mRNA.  
 DR HSBP; P00974; 1BP1.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.  
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro; IPR008296; Prot\_inh\_TFPI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF; PIRSF001620; TFPI; 1.  
 DR PRINTS; PR00759; BASICTPASE.  
 DR ProDom; PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 224 AA; 25538 MW; 11C2D1C6C789445B CRC64;

Query Match 48.6%; Score 635; DB 2; Length 224;  
 Best Local Similarity 53.5%; Pred. No. 9e-50;  
 Matches 107; Conservative 35; Mismatches 50; Indels 8; Gaps 4;

QY 28 PGNNAEICLPDYPGCRALIRYTYDRYQSCROFLYGGCGGNANFYTWACDADCM 87  
 DB 22 PMQGNITVCLLPDDEGPKCALIPHYTYDRYTCQGFYGGCGGNANFYTWACDADCM 81  
 QY 88 RIEKVPKVCRLQVSDVDDCGESTKCYFNLSSMTCKEFPSSGCHRRRIENRPDEATCMG 147  
 DB 82 KIKKVPKACRM-VPDGCPGRGTYKRYAYNMKTRCQGFYGGCYGN--DNNPDQDSCIN 138  
 QY 148 FCAPKK-IPSPCYSPKDEGLCSANVTYRYFNPRTYTCDAFTYTGCGGDNFNFSREDCKR 206  
 DB 139 FCAPRDAPSPCYSPKDEGSCASVTRTYFNIESKACEFYTTGCGGNNFNFSREDCKR 198  
 QY 207 ACAKALKKKK---KMPKLR 222  
 DB 199 VCKKGTGRPRNPKIRIR 218

RESULT 9  
 OSFYV6\_XENTR PRELIMINARY; PRT; 219 AA.  
 AC OSFYV6;  
 DT 10-MAY-2005 (Tremblrel. 30, Created)  
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)  
 DE MGCL08301 protein.  
 GN Name=MGCL08301;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Batelaeostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus; Silurana.  
 CX NCBI\_Taxid=8364;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Whole body;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Haleh P.,  
 RA Diatchenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,  
 RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhe D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2].  
 RN NCUTEOTIDE SEQUENCE.  
 RP TISSUE=Whole body;  
 RC Klein S., Gerhard D.S.;  
 RA Submitted (Feb-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
 DR EMBL; BC089705; AAH9705.1; -; mRNA.  
 DR GO; GO:0005576; C:extracellular region; IEA.  
 DR GO; GO:0030414; F:protease inhibitor activity; IEA.  
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR InterPro; IPR008296; Prot\_inh\_TFPI.  
 DR Pfam; PF00014; Kunitz\_BPTI; 3.  
 DR PIRSF; PIRSF001620; TFPI; 1.  
 DR PRINTS; PR00759; BASICTPASE.  
 DR ProDom; PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
 DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
 SQ SEQUENCE 219 AA; 24949 MW; 8F6AD89B8556C8 CRC64;

Query Match 48.2%; Score 630; DB 2; Length 219;  
 Best Local Similarity 52.7%; Pred. No. 2.5e-49;  
 Matches 108; Conservative 35; Mismatches 54; Indels 8; Gaps 4;

QY 28 PGNNAEICLPDYPGCRALIRYTYDRYQSCROFLYGGCGGNANFYTWACDADCM 87  
 DB 21 PMQGNITVCLLPDDEGPKCALIPHYTYDRYTCQGFYGGCGGNSNFKLSMEDCKEPCM 80  
 QY 88 RIEKVPKVCRLQVSDVDDCGESTKCYFNLSSMTCKEFPSSGCHRRRIENRPDEATCMG 147  
 DB 81 KIKKVPKACRM-VPDGPGRGTYKRYAYNMKTRCQGFYGGCYGN--DNNPDQDSCIN 137  
 QY 148 FCAPKK-IPSPCYSPKDEGLCSANVTYRYFNPRTYTCDAFTYTGCGGDNFNFSREDCKR 206  
 DB 138 FCAPRDAPSPCYSPKDEGSCASVTRTYFNIESKACEFYTTGCGGNNFNFSREDCKR 197  
 QY 207 ACAKALKKKKMPKLRPSIRKIR 231  
 DB 198 VC---KKGSRPRNRIRIRVRIQ 218

RESULT 10  
 QARDL7\_TETNG PRELIMINARY; PRT; 190 AA.  
 AC QARDL7;  
 DT 13-SEP-2005 (Tremblrel. 31, Created)  
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)  
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAF16203, whole genome shotgun sequence.

ORNNames=GSTENG00038126001.  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontinae; Tetraodon.  
 OX NCBI\_TaxId=99863;  
 RN [1]  
 RP Nucleotide sequence.  
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 Micaud E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 Marcel S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 Daetwyler C., Salanoubat M., Ley M., Boudet N., Castellan S.,  
 RA Anthouard V., Udin C., Castelli L., Katinka M., Vacherie B.,  
 Blemont C., Skallil Z., Catroilo L., Poulsen J., De Bernardinis V.,  
 RA Crand C., Duprat S., Chaptier P., Coutanceau J.P., Guzy J.,  
 Parra G., Landier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Gulgo R., Zody M.C., Mesirov J.,  
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Landet P., Schachter V., Queller F., Saurin W., Scarpelli C.,  
 RA Winkler P., Landier B.S., Weissbach J., Roest Croillius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP Nucleotide sequence.  
 RG Genoscope, Whitehead Institute Centre for Genome Research,  
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC -!- SIMILARITY: Contains 3 BPT1/Kunitz inhibitor domains.  
 DR EMBL; CAE01016203; CAG13515.1; -; Genomic\_DNA.  
 DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
 DR Pfam; PF00014; Kunitz\_BPT1\_3.  
 DR PRINTS; PR00759; BASICPRASE.  
 DR ProDom; PD000222; Prot\_inh\_Kunz-m; 3.  
 DR SMART; SM00131; KU; 3.  
 DR PROSITE; PS00280; BPT1\_KUNITZ\_1; 2.  
 DR PROSITE; PS0279; BPT1\_KUNITZ\_2; 3.  
 SQ SEQUENCE 190 AA, 21614 MW, 8AEE6C5515605BCD CRC64;  
  
 Query Match 35.1%; Score 458; DB 2; Length 190;  
 Best Local Similarity 47.6%; Pred. No. 1.1e-33;  
 Matches 79; Conservative 28; Mismatches 55; Indels 4; Gaps 3;  
  
 Oy ICILPDLVGPGRALLRRTYDRYRQSCGFPLVGGCGEAGANNYYTAEADDDCMRTKXPX 94  
 Db 26 VCLLVQVNGPGRGIDERTYRNTYTKCBIFSYGGCGGANNRRSRFOCKTFRPKIPQ 85  
 Oy 95 VCRLLQVSDDOCGESTKXFPVLSSMTCEKFPFSGGCHNRIRIENRPDEATCMGPCAP-KK 153  
 Db 86 ICRPFQER-GECRALLRKTFPMTTMOCEPFFYGGCLGS--SNKDDDLASCRCYCSPIKS 142  
 Oy 154 IPSFCYSBKDEGLCSANVTRYFNRPYRTCDAFYTYGCGGNDNNFV 199  
 Db 143 LPVLCLDPLDKGKGSASPFRYYNNATYKKCEEFYISGGCGNSKNFV 188  
  
 RESULT 11  
 OSR98 PONPY PRELIMINARY; PRT; 304 AA.  
 ID OSR98 PONPY  
 AC OSR98  
 DT 01-FEB-2005 (Tremblrel. 29, Created)  
 DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)  
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)  
 DE Hypothetical protein DKFZp469B1122.  
 GN Name=DKFZp469B1122;  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
 OC Pongo.  
 OX NCBI\_TaxId=9600;

Query	Match	30.3%	Score 396	DB 2	Length 304
Best Local Similarity	30.6%	Pred. No. 8e-28			
Matches	87	Conservative 37	Mismatches 84	Indels 76	Gaps 8
QY	12	LLPLPTEALDGAOEPFYGNNA-----ETCLPLDVGPCRALLRYYDHYT	58		
DB	17	LLNLNAPPLNADSEBDEGHITITDTBLPLKMHSPFCAFRADDPCCALMKRFFNFT	76		
QY	59	QSCROPLTGGCGGNANNFYTWBACDDACMR-----IRKPYKCRLOVSYDQ--	105		
DB	77	RCQCEFFITGGCGEGNRRFESBLECCQKMTNRNANKIKITTLQGEKEDPCPLE--EDGPI	133		
QY	106	CEGSTETKYPNLSMWTCKEFPSSGGCHRRIRIENRFPDEATCNGFC-----	149		
DB	134	CRGVITRFYNNQTKQGERFKYGGCLGNM--NNFETLSECKNTCEDGPNQVDNYGTOL	191		
QY	150	-----APKCI-----PSCYSPKOBGLCSANVTYTYFNRPRITCDAPFYTGG	192		
DB	192	NAGNNSLTPOSTKVPSLPEFHPGSPWCLTPADRGLCRAENENRPNYSVIGKCRPFYSGG	251		
QY	193	GNDNNFVSREDOCKRACAKAL-----KKGKMPKLRFA	224		
DB	252	GNENFTSKQECRLCKKGTGFIQIRISKGLITKRRKQKQRYKIA	295		
RESULT 12					
TFPII HUMAN					
ID	TFPII_HUMAN	STANDARD	PRT	304 AA	
AC	P10646; O95103;				
DT	01-JUL-1989 (Rel. 11, Created)				
DT	01-JUL-1989 (Rel. 11, Last sequence update)				
DT	13-SEP-2005 (Rel. 46, Last annotation update)				
DE	Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-				
DE	associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor				
DE	(BPI).				
GN	Name=TFPI; Synonym=LAZI, TFPII;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Buthera; Eutarchontoglires; Primates; Catarrhini; Homidae;				
OC	Homo				
OK	NCBI_TaxID=9606;				
OK	[1]				
RN	NP_001127				
RP	NCBI_TaxID=9606				
RX	Medline=88198127; PubMed=2452157;				
RA	Mun T.-C., Kretzner K.K., Girard T.J., Miletich J.P., Brose G.J. Jr.;				
RT	"cloning and characterization of a cDNA coding for the lipoprotein-				
RT	associated coagulation inhibitor shows that it consists of three				

- RT tandem Kunitz-type inhibitory domains.";  
RL J. Biol. Chem. 263:6001-6004(1988).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=9112927; PubMed=1993173;  
RA van der Logt C.P.B., Reitema P.H., Bertina R.M.;  
RT "Intron-exon organization of the human gene coding for the  
RT lipoprotein-associated coagulation inhibitor: the factor Xa dependent  
RT inhibitor of the extrinsic pathway of coagulation.";  
RL Biochemistry 30:1571-1577(1991).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=91161593; PubMed=2002045;  
RA Girard T.J., Eddy R., Wesselschmidt R.L., Macphail L.A., Likert K.M.,  
RA Byers M.G., Shows T.B., Broze G.J. Jr.;  
RT "Structure of the human lipoprotein-associated coagulation inhibitor  
RT gene. Intron/exon gene organization and localization of the gene to  
RT chromosome 2.";  
RL J. Biol. Chem. 266:5036-5041(1991).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=93388722; PubMed=2781520; DOI=10.1016/0049-3848(89)90454-4;  
RA Girard T.J., Warren L.A., Novotny W.F., Bejcek B.E., Miletich J.P.,  
RA Broze G.J. Jr.;  
RT "Identification of the 1.4 kb and 4.0 kb messages for the lipoprotein  
RT associated coagulation inhibitor and expression of the encoded  
RT protein.";  
RL Thromb. Res. 55:37-50(1988).  
RN [5]  
RP NUCLEOTIDE SEQUENCE (ISOFORM BETA).  
RX Chang J.-Y., Monroe D.M., Roberts H.R.;  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).  
RA Rieder M.J., Carrington D.P., da Ponte S.H., Haecings N.C.,  
RA Ahearn M.O., Kildanek S.A., Rajkumar N., Toth E.J., Yi Q.,  
RA Nickerson D.A.;  
RT "SeacatSNP: NHLBI HL6682 program for genomic applications, UW-  
RT FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM BETA).  
RC TISUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toehlyuk S., Carninci P., Prange C.,  
RA Bosh S.A., McMan P.J., McKernan K.J., Abramson R.D., Millhys S.J.,  
RA Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodrigues Y., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield J.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [8]  
RP PROTEIN SEQUENCE OF 29-50.  
RX MEDLINE=90036996; PubMed=2553722;  
RA Novotny W.F., Girard T.J., Miletich J.P., Broze G.J. Jr.;  
RT "Purification and characterization of the lipoprotein-associated  
RT coagulation inhibitor from human plasma.";  
RL J. Biol. Chem. 264:18832-18837(1989).  
RN [9]  
RP PROTEIN SEQUENCE OF 29-43.  
RX PubMed=15340161; DOI=10.1110/ps.04682504;  
RA Zhang Z., Henzel W.J.;  
RT "Signal peptide prediction based on analysis of experimentally  
RT verified cleavage sites.";  
RL Protein Sci. 13:2819-2824(2004).  
RN [10]  
RP INHIBITORY SITES.  
RX MEDLINE=99181950; PubMed=2927510; DOI=10.1038/336518a0;  
RA Girard T.J., Warren L.A., Novotny W.F., Likert K.M., Brown S.G.,  
RA Miletich J.P., Broze G.J. Jr.;  
RT "Functional significance of the Kunitz-type inhibitory domains of  
RT lipoprotein-associated coagulation inhibitor.";  
RL Nature 338:518-520(1989).  
RN [11]  
RP CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=96224851; PubMed=8639592; DOI=10.1021/bj9524880;  
RA Nakahara Y., Miyata T., Hamuro T., Funatsu A., Miyagi M.,  
RA Terasawa S., Kato H.;  
RT "Amino acid sequence and carbohydrate structure of a recombinant human  
RT tissue factor pathway inhibitor expressed in Chinese hamster ovary  
RT cells: one N- and two O-linked carbohydrate chains are located between  
RT Kunitz domains 2 and 3 and one N-linked carbohydrate chain is in  
RT Kunitz domain 2.";  
RL Biochemistry 35:6450-6459(1996).  
RN [12]  
RP REVIEW.  
RX MEDLINE=91104709; PubMed=2271516;  
RA Broze G.J. Jr., Girard T.J., Novotny W.F.;  
RT "Regulation of coagulation by a multivalent Kunitz-type inhibitor.";  
RL Biochemistry 29:7539-7546(1990).  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 121-178 IN COMPLEX WITH  
RP TRYPSIN.  
RX MEDLINE=97390427; PubMed=9242660; DOI=10.1074/jbc.272.32.19931;  
RA Stubbs M.T., Morenweiser R., Stuerzbecher J., Bauer M., Bode W.,  
RA Huber R., Plechotcka G.P., Matchner G., Sommerhoff C.P., Fritz H.,  
RA Auerwald R.A.;  
RT "The three-dimensional structure of recombinant leech-derived trypsin  
RT inhibitor in complex with trypsin. Implications for the structure of  
RT human mast cell trypsinase and its inhibition.";  
RL J. Biol. Chem. 272:19931-19937(1997).  
RN [14]  
RP STRUCTURE BY NMR OF 121-182.  
RX MEDLINE=9742711; PubMed=9199408; DOI=10.1006/jmbi.1997.1029;  
RA Burgering M.J.M., Orbone L.P.M., van der Doelen A., Milders J.,  
RA Theunissen H.J.M., Groenenhuis P.D.J., Bode W., Huber R., Stubbs M.T.;  
RT "The second Kunitz domain of human tissue factor pathway inhibitor:  
RT cloning, structure determination and interaction with factor Xa.";  
RL J. Mol. Biol. 269:395-407(1997).  
RN [15]  
RP STRUCTURE BY NMR OF 210-270.  
RX MEDLINE=21633982; PubMed=11772005; DOI=10.1021/bi011299g;  
RA Mine S., Yamazaki T., Miyata T., Hara S., Kato H.;  
RT "Structural mechanism for heparin-binding of the third Kunitz domain  
RT of human tissue factor pathway inhibitor.";  
RL Biochemistry 41:78-85(2002).  
RN [16]  
RP VARIANT MET-292.  
RX MEDLINE=99318093; PubMed=10391209; DOI=10.1038/10290;  
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemes J., Zlaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
RA Lander E.S.;  
RT "Characterization of single-nucleotide polymorphisms in coding regions  
RT of human genes.";  
RL Nat. Genet. 22:231-238(1999).  
RN [17]  
RP ERRATUM.  
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
RA Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemes J., Zlaugra L.,  
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
RA Lander E.S.;  
RT Nat. Genet. 23:373-373(1999).



```

CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent
CC way, inhibits VIIa/cisase factor activity, presumably by forming a
CC quaternary Xa/LaCII/VIIa/TF complex. It possesses an antithrombotic
CC action and also the ability to associate with lipoproteins in
CC plasma.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha; Synonym=alpha;
CC IsoId=PI0646-1; Sequence=displayed;
CC Name=Beta; Synonym=beta;
CC IsoId=PI0646-2; Sequence=VSP_003030, VSP_003031;
CC -1- TISSUE SPECIFICITY: Mostly in endothelial cells.
CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The
CC first domain interacts with VIIa and TF, the second one with Xa.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL, J03225; AAA52022.1; -; mRNA.
CC EMBL, M58650; AAA59480.1; -; Genomic_DNA.
CC EMBL, M58645; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58645; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58646; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58647; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58648; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M58649; AAA59480.1; JOINED; Genomic_DNA.
CC EMBL, M59459; AAA59526.1; -; Genomic_DNA.
CC EMBL, M59493; AAA59526.1; JOINED; Genomic_DNA.

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Best Local Similarity 30.3%; Pred. No. 4,3e-27;
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

QY 12 LLLFLTEALGDAOE-----PTGNNAICLLPLDYGPCALLLRYYDRYT 58
DB 17 LLLNLAAPPLNDSBDEBHTIITDTLPPLKLMHSPCAFKADDPCKAIMKRPFFNIPT 76
QY 59 QSCRQPLVGGCGGNANFFTWAEACDCAWR-----IKVPKVCRLQVSDQ-- 105
DB 77 RCCEFTIYGGCGGNORFESLEBCKKMCYRDANRIKTTLOQKXDPFCFLR---EDPGI 133
QY 106 CGSTKTYFFNLSTMTCKEFPFGSGCHRNRIENRPDEATCMGFC----- 149
DB 134 CRGYITRYFYNNQTKQCEKRFYGGCLGNM--NNFETLEBCKNI CDGPGNGPOVDNYGTOL 191
QY 150 -----APKCI-----PSFCYSPKDGCLGSANTRYYPNRYTCDAFTYTGCG 192
DB 192 NNVNNSLTQSTKVPSELFEHGPSWCLTPADGCLCRANENRFFYNVSVIGKCPFKYSGCG 251
QY 193 GNDNPFVSRDECKRACAKAL-----KKKKKMPKLRPA 224
DB 252 GHENNFTSKQBCLRACKGKGFQIRISKGGLIKTKRKRRKQKRVKIA 295

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DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DB Hypothetical protein TPPI.
GN Name=TPPI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.

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OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Boutine S., Stoneking T., Phillips A.;
RT "The sequence of Homo sapiens HAC clone RP11-432D12."
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (Jun-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (Sep-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
CC EMBL, AC007319; AA14807.1; -; Genomic_DNA.
CC GO, GO:0005576; C:extracellular region; IEA.
CC GO, GO:0004867; F:proteinase inhibitor activity; IEA.
CC GO, GO:0007596; P:blood coagulation; IEA.
CC Hypothetical protein.
SQ SEQUENCE 304 AA; 35015 MW; 5281B32B758B44FE CRC64;

Query Match      29.7%; Score 388; DB 2; Length 304;
Best Local Similarity 30.3%; Pred. No. 4,3e-27;
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;

QY 12 LLLFLTEALGDAOE-----PTGNNAICLLPLDYGPCALLLRYYDRYT 58
DB 17 LLLNLAAPPLNDSBDEBHTIITDTLPPLKLMHSPCAFKADDPCKAIMKRPFFNIPT 76
QY 59 QSCRQPLVGGCGGNANFFTWAEACDCAWR-----IKVPKVCRLQVSDQ-- 105
DB 77 RCCEFTIYGGCGGNORFESLEBCKKMCYRDANRIKTTLOQKXDPFCFLR---EDPGI 133
QY 106 CGSTKTYFFNLSTMTCKEFPFGSGCHRNRIENRPDEATCMGFC----- 149
DB 134 CRGYITRYFYNNQTKQCEKRFYGGCLGNM--NNFETLEBCKNI CDGPGNGPOVDNYGTOL 191
QY 150 -----APKCI-----PSFCYSPKDGCLGSANTRYYPNRYTCDAFTYTGCG 192
DB 192 NNVNNSLTQSTKVPSELFEHGPSWCLTPADGCLCRANENRFFYNVSVIGKCPFKYSGCG 251
QY 193 GNDNPFVSRDECKRACAKAL-----KKKKKMPKLRPA 224
DB 252 GHENNFTSKQBCLRACKGKGFQIRISKGGLIKTKRKRRKQKRVKIA 295

RESULT 14
ID TPPI1_RABIT STANDARD; PRT; 300 AA.
AC P19761; Q28828;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-
DB associated coagulation inhibitor) (LACI) (Extrinsic pathway inhibitor)
DB (BPTI).
GN Name=TPPI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINB=91057146; PubMed=2136251;
RA Wesselschmidt R.L., Girard T.J., Broze G.J. Jr.;

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RT "cDNA sequence of rabbit lipoprotein-a-associated coagulation  
inhibitor.";  
RT Nucleic Acids Res. 18:6440-6440(1990).  
RN [2]  
RP SEQUENCE REVISION TO 72; 211 AND 218.  
RC TISSUE=Liver;  
RX MEDLINE=92335027; PubMed=1630940;  
RA Warn-Cramer B.J., Broze G.J. Jr., Komives E.A.;  
RT "cDNA sequence of rabbit tissue factor pathway inhibitor.";  
RL Nucleic Acids Res. 20:3548-3548(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung;  
RX MEDLINE=93276427; PubMed=8503123; DOI=10.1016/0049-3848(93)90059-W;  
RA Belaroun J., Kuppawamy M.N., Birkoft J.J., Bajaj S.P.;  
RT "Revised cDNA sequence of rabbit tissue factor pathway inhibitor.";  
RL Thromb. Res. 69:547-553(1993).  
CC -1- FUNCTION: Inhibits factor X (X(a)) directly and, in a Xa-dependent  
way, inhibits VIIa/tissue factor activity, presumably by forming a  
ternary Xa/LaCl/VIIa/TF complex. It possesses an antithrombotic  
action and also the ability to associate with lipoproteins in  
plasma.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- DOMAIN: This inhibitor contains three inhibitory domains. The  
first domain interacts with VIIa and TF, the second one with Xa  
(By similarity).  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
-----  
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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
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CC EMBL; X54708; CAA38515.1; ALT SEQ; mRNA.  
CC PIR; I46937; I46937.  
CC HSRP; P10646; ITRX.  
CC SMR; P19761; 117-173, 207-266.  
CC InterPro; IPR002223; Prot\_inh\_Kunz-m.  
CC InterPro; IPR008296; Prot\_inh\_TFPI.  
CC Pfam; PF00014; Kunitz\_BPTI; 3.  
CC PIRSF; PIRSF001620; TFPI; 1.  
CC PRINTS; PR00759; BASICPTASE.  
CC ProDom; PD000222; Prot\_inh\_Kunz-m; 3.  
CC PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
CC PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
CC Blood coagulation; Glycoprotein; Protease inhibitor; Repeat;  
KW Serine protease inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 300 Tissue factor pathway inhibitor.  
FT DOMAIN 50 100 BPTI/Kunitz inhibitor 1.  
FT DOMAIN 121 171 BPTI/Kunitz inhibitor 2.  
FT DOMAIN 213 263 BPTI/Kunitz inhibitor 3.  
FT SITE 60 61 Reactive bond (By similarity).  
FT SITE 131 132 Reactive bond (By similarity).  
FT SITE 223 224 Reactive bond (By similarity).  
FT CARBOHYD 141 141 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 191 191 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 252 252 N-linked (GlcNAc...) (potential).  
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FT DISULFID 59 83 By similarity.  
FT DISULFID 75 96 By similarity.  
FT DISULFID 121 171 By similarity.  
FT DISULFID 130 154 By similarity.  
FT DISULFID 146 167 By similarity.  
FT DISULFID 263 263 By similarity.  
FT DISULFID 222 246 By similarity.  
FT DISULFID 238 259 By similarity.  
FT CONFLICT 31 31 Missing (in Ref. 3).  
FT CONFLICT 269 272 PKSI -> RNLS (in Ref. 3).  
FT SEQUENCE 300 AA; 34436 MW; A08DE36537708CA6 CRC64;

Query Match 29.7%; Score 387.5; DB 1; Length 300;  
Best Local Similarity 30.7%; Pred. No. 4.7e-27;  
Matches 89; Conservative 31; Mismatches 73; Indels 97; Gaps 8;  
QY 12 LLLPTEALGDPAAB-----PTGNNAICLLPDPYGCRAALLRYVD 55  
DB 13 LLLGLVPAVSSAAEDDEFTYITDIKPPLOKPTIS---FCMKVDDGFCRAIYIKRFPN 69  
QY 56 RYTOGCRPLYGCGCGNANNFYWEACDACMR-----IEKVPRV 95  
DB 70 ILTHQCEBRYGCGENRFRFSLBCKBKCARDPKMTTKLTPOKGRDPCFLBSPGI 129  
QY 96 CRLQVSDQCGSGIEKTPFNLSSMTCKPFBGCGRRRIERPFDEATCMFC----- 149  
DB 130 CR-----GYITRFYNNQSKQCBFRYKGGCLGML--NNFSLBCKKNTCENPTSD 177  
QY 150 -----APKXI-----PSPCYSPKDEGLSANTRYYPNRYRT 182  
DB 178 FOVDHRTQTLVNTNLINOPTKAPRRNAFHGSPCLPPADNGLCQANEIRFPYNAIICK 237  
QY 183 CDAPFTYGGGNDNNFVSRBDCKRACAYAL-----KXKCKAP 219  
DB 228 CRPFYSGCGGNENFTSKACITACKKGFIPKSIKGLIKTKRKKKQP 287

RESULT 15  
093424 CYPCA PRELIMINARY; PRT; 287 AA.  
ID 093424 CYPCA PRELIMINARY; PRT; 287 AA.  
AC 093424;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxId=7962;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RA Gracey A.V.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.  
CC EMBL; AF008648; AAC19410.1; -; mRNA.  
DR HSRP; P31713; ISHP.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0010414; F:protease inhibitor activity; IEA.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.  
DR GO; GO:0007536; F:blood coagulation; IEA.  
DR InterPro; IPR002223; Prot\_inh\_Kunz-m.  
DR InterPro; IPR008296; Prot\_inh\_TFPI.  
DR Pfam; PF00014; Kunitz\_BPTI; 3.  
DR PIRSF; PIRSF001620; TFPI; 1.  
DR PRINTS; PR00759; BASICPTASE.  
DR ProDom; PD000222; Prot\_inh\_Kunz-m; 3.  
DR SMART; SM00131; KU; 3.  
DR PROSITE; PS00280; BPTI\_KUNITZ\_1; 3.  
DR PROSITE; PS0279; BPTI\_KUNITZ\_2; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 287 AA; 33093 MW; DF69B3D767181158 CRC64;  
Query Match 29.6%; Score 387; DB 2; Length 287;  
Best Local Similarity 35.0%; Pred. No. 5e-27;  
Matches 85; Conservative 23; Mismatches 71; Indels 64; Gaps 7;  
QY 36 CLLPDYGPCALLIRYDRYTOGCRPLYGCGCGNANNFYWEACDACM-RLEKVPK 94  
DB 42 CALKQDBGPCALIKDRFYFDYDTGRCSBFRYGGCGGNENNFETLOECCEKMLVKEDKSP- 100  
QY 95 VCRLOVSDVDDO---CEGSTEKYPFNLSSMTCKPFBGCGCHNRRIENRPPDEATCMGFCAP 151  
DB 101 -COL---DDEPGCPKGLVPRYFFDFKSOBCRFRFYGGCGFN--ANNRTIKYCHERCLP 153

Qy	152	-----	KK----	IPFCY	159
Db	154	ALNNMRNAPLKPEBBEAKPTEPLAKHVEAPLNASHLPWQRNSKPSAKKPRLNRPKLCF			213
Qy	160	SPRDEGLCSANVTYYYFNPRYRTCDAPTYTGCGNDNNFVSRREDCKRACAKLKKKKMP			219
Db	214	SPIDRGNCESGGRMYNPRTKRCOMFHSGCCGNKNNFVXRGDCIKMCMRDLRRKILRL			273
Qy	220	KLR	222		
Db	274	KLR	276		

Search completed: March 9, 2006, 19:56:47  
Job time : 232 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:57:04 ; Search time 47 Seconds

(without alignments)  
413.378 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306  
Sequence: 1 MDPARPLGSLILLPLTREA.....KMPKLRPASNRIRKIRKQF 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5 COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/7 COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/RB\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	1 US-08-147-710-2	Sequence 2, Appl1
2	1306	100.0	235	1 US-08-458-090-2	Sequence 2, Appl1
3	1306	100.0	235	1 US-08-457-887-2	Sequence 2, Appl1
4	1306	100.0	235	2 US-08-817-145-3	Sequence 3, Appl1
5	1306	100.0	235	2 US-09-702-705-332	Sequence 332, App
6	1306	100.0	235	2 US-09-736-457-332	Sequence 332, App
7	1306	100.0	235	2 US-09-614-1248-332	Sequence 332, App
8	1306	100.0	235	2 US-09-904-621-2	Sequence 2, Appl1
9	1306	100.0	235	2 US-09-671-325-332	Sequence 332, App
10	1306	100.0	235	2 US-09-589-184-332	Sequence 332, App
11	1306	100.0	235	2 US-09-658-824-332	Sequence 332, App
12	1306	100.0	235	2 US-09-949-016-6735	Sequence 6735, App
13	1306	100.0	235	2 US-10-017-754-332	Sequence 332, App
14	1306	100.0	235	2 US-09-651-563-332	Sequence 332, App
15	1306	100.0	235	2 US-09-519-642-332	Sequence 332, App
16	1306	100.0	235	2 US-09-949-016-7058	Sequence 7058, App
17	1200	91.9	213	1 US-08-796-850-2	Sequence 2, Appl1
18	1200	91.9	213	1 US-09-766-778-2	Sequence 2, Appl1
19	1200	91.9	213	2 US-10-086-176A-6	Sequence 6, Appl1
20	394.5	30.2	291	2 US-10-000-489-48	Sequence 48, Appl1
21	393.5	30.1	291	2 US-10-000-489-52	Sequence 52, Appl1
22	388	29.7	304	1 US-08-026-145-2	Sequence 2, Appl1
23	388	29.7	304	1 US-08-446-646-9	Sequence 9, Appl1
24	388	29.7	304	1 US-08-676-125A-18	Sequence 18, Appl1
25	388	29.7	304	1 US-09-136-012A-18	Sequence 18, Appl1
26	388	29.7	304	2 US-08-676-124-1	Sequence 1, Appl1
27	388	29.7	304	2 US-08-208-264A-25	Sequence 25, Appl1

28	388	29.7	304	2 US-09-414-878-1	Sequence 1, Appl1
29	388	29.7	304	2 US-09-240-136-1	Sequence 1, Appl1
30	388	29.7	304	2 US-09-421-097-25	Sequence 25, Appl1
31	388	29.7	304	2 US-09-638-770A-1	Sequence 1, Appl1
32	388	29.7	304	2 US-09-054-272-16	Sequence 16, Appl1
33	388	29.7	304	2 US-10-167-351-1	Sequence 1, Appl1
34	388	29.7	304	6 546783-2	Patent No. 546783
35	388	29.7	381	2 US-09-949-016-7400	Sequence 7400, App
36	387.5	29.7	276	1 US-08-437-841-9	Sequence 9, Appl1
37	387.5	29.7	276	1 US-08-286-521-9	Sequence 9, Appl1
38	387.5	29.7	276	1 US-08-436-175-9	Sequence 9, Appl1
39	387.5	29.7	276	2 US-08-854-764-3	Sequence 9, Appl1
40	387.5	29.7	276	2 US-08-943-682-9	Sequence 9, Appl1
41	387.5	29.7	276	2 US-09-741-106-9	Sequence 9, Appl1
42	387.5	29.7	276	4 PCT-US95-09377-3	Sequence 3, Appl1
43	387.5	29.7	276	4 PCT-US95-09464-9	Sequence 9, Appl1
44	384.5	29.4	213	6 546783-25	Patent No. 546783
45	384.5	29.4	276	1 US-08-796-850-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-147-710-2  
; Sequence 2, Application US/08147710  
; Patent No. 5455338  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Kistel, Walter  
; APPLICANT: Foster, Donald C.  
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
; TITLE OR INVENTION: METHODS RELATING THERETO  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSES: ZymoGenetics, Inc.  
; STREET: 4225 Roosevelt Way, N.E.  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,710  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, Gary E  
; REGISTRATION NUMBER: 31-684  
; REFERENCE/DOCKET NUMBER: 93-14  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-547-8080 ext 322  
; TELEFAX: 206-548-2329  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 235 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-147-710-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLPLTREAAGDAQEPFGNNNAICLLPLVDGPGCAALLRYRDRYTOS 60  
DB 1 MDPARPLGSLILLPLTREAALGDAAQEPFGNNNAICLLPLVDGPGCAALLRYRDRYTOS 60

QY 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
DB 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
QY 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235  
DB 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235

RESULT 2  
US-08-458-090-2  
Sequence 2, Application US/08458090  
Patent No. 5728674  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: METHODS RELATING THERETO  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458, 090  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-1402  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-458-090-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLLPLDYGPCRALLLRYYDRYQS 60  
DB 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLLPLDYGPCRALLLRYYDRYQS 60  
QY 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
DB 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
QY 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235  
DB 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235

DB 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235

RESULT 3  
US-08-457-887-2  
Sequence 2, Application US/08457887  
Patent No. 5914315  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: METHODS RELATING THERETO  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,887  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-1401  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-457-887-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLLPLDYGPCRALLLRYYDRYQS 60  
DB 1 MDPARPLGISLILFLTEALGDAQAQEPYGNNAEICLLPLDYGPCRALLLRYYDRYQS 60  
QY 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
DB 61 CROPLVGGCEGNANNTYTWACDCAWRIEKVKVCRLOVSVDDQCEGSTEKTFPNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPFCYSPDCEGCSANVTTRYFNPRY 180  
QY 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235  
DB 181 RTCDATYTGCGGNDNNFVSREDCKRACAKALKKKKKMPKLPFASIRIRIKRKQF 235  
RESULT 4  
US-08-817-145-3  
Sequence 3, Application US/08817145  
Patent No. 6025329  
GENERAL INFORMATION:  
APPLICANT: Utsomi, Jun  
APPLICANT: Sudo, Tetsuo



APPLICANT: TANAKA, Yasuhiko  
APPLICANT: MATSUI, Mizuo  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC  
DISEASES  
TITLE OF INVENTION: DISEASES  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Birch, Stewart, Kolaesch & Birch, LLP.  
STREET: P.O. Box 747  
CITY: Falls Church  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/817,145  
FILING DATE: 02-JUL-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 760-230P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-817-145-3

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
QY 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120  
DB 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120  
QY 121 TCEKPFSSGCHNRRIENRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
DB 121 TCEKPFSSGCHNRRIENRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
QY 181 RTCDAFTYTCGGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235  
DB 181 RTCDAFTYTCGGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235

RESULT 5  
US-09-702-705-332  
Sequence 332, Application US/09702705  
Patent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaltanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C14  
CURRENT APPLICATION NUMBER: US/09/702,705  
CURRENT FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 1833  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-702-705-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
QY 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120  
DB 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120  
QY 121 TCEKPFSSGCHNRRIENRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
DB 121 TCEKPFSSGCHNRRIENRPPDRTCMGFCAPKKIISFCYSPDDEGLCSANTVRYFNPRY 180  
QY 181 RTCDAFTYTCGGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235  
DB 181 RTCDAFTYTCGGGNDNNFVSRDCKRAKAKLKKKKKMPKLPASIRIRIRKKQF 235

RESULT 6  
US-09-736-457-332  
Sequence 332, Application US/09736457  
Patent No. 6509448  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaltanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C15  
CURRENT APPLICATION NUMBER: US/09/736,457  
CURRENT FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 1864  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-736-457-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAAOEPGNNABICLLPLDYGPCRALILRYYYDRYTOS 60  
QY 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120  
DB 61 CRQFLYGGCGEGNANNFYTWACDCAWRIEKVPKVCRLQVSDDCGSGSTKXFFNLSSM 120

Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235

RESULT 7  
US-09-614-124B-332  
Sequence 332, Application US/09614124B  
Patent No. 6630574

GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Ranger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C9  
CURRENT APPLICATION NUMBER: US/09/614,124B  
CURRENT FILING DATE: 2001-07-11  
NUMBER OF SEQ ID NOS: 1668  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-614-124B-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Db 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Qy 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Db 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235

RESULT 8  
US-09-904-621-2  
Sequence 2, Application US/09904621  
Patent No. 6656746

GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/09/904,621  
CURRENT FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338

PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-904-621-2

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Db 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Qy 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Db 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Qy 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235  
Db 181 RTCDATYTGCGGNDNNFVSRDECKRACAKALKKKKKMPKLRFASIRIRIRKKQF 235

RESULT 9  
US-09-671-325-332  
Sequence 332, Application US/09671325  
Patent No. 6667154

GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodges, Michael A.  
APPLICANT: Ranger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.478C12  
CURRENT APPLICATION NUMBER: US/09/671,325  
CURRENT FILING DATE: 2000-09-26  
NUMBER OF SEQ ID NOS: 1825  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-671-325-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Db 1 MDPARPLGISILLFLTEALGDAAQEPYGNNAEICLLPLDYGPCRALLRYYDRYTOS 60  
Qy 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Db 61 CROFLYGCGEGNANNFYWEACDDACWRIEKVPKVCRLQVSYDDQCEGSTTEKFFNLISM 120  
Qy 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180  
Db 121 TCEKFSGGCHNRNLENRPDEATCMGFCAPKKIPSCFVSPKDEGLCSANVTTRYFNPRY 180

Oy 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235  
Db 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235

RESULT 10  
US-09-589-184-332  
Sequence 332, Application US/09589184  
Patent No. 6686447  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chahtanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Panger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C8  
CURRENT APPLICATION NUMBER: US/09/589,184  
CURRENT FILING DATE: 2000-06-05  
NUMBER OF SEQ ID NOS: 827  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-589-184-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Db 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235  
Db 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235

RESULT 11  
US-09-658-824-332  
Sequence 332, Application US/09658824  
Patent No. 6746846  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chahtanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Panger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Darlick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C11  
CURRENT APPLICATION NUMBER: US/09/658,824  
CURRENT FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 1788  
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-658-824-332

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Db 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235  
Db 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235

RESULT 12  
US-09-949-016-6735  
Sequence 6735, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6735  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6735

Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2e-123;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Db 1 MDPAPPLGISILLFLTEALGDAAOEPYGNNAEICLLPLDYGPCRALLLRYRYRYS 60  
Oy 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Db 61 CRQPLYGCGEGNANFYTWACDDACWRIEKPVKYCRLOVSYDDOCESGTERKYPNLSM 120  
Oy 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Db 121 TCEKPFSGGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPDEGLCSANVTRYFNPXY 180  
Oy 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235  
Db 181 RTCDATYTGCGGNNNFVSRDCRACAKALKKKKKMPKJAFASIRIRIRKKOF 235

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RESULT 13
US-10-017-754-332
Sequence 332, Application US/10017754
Patent No. 6858304
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tonglong
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Derrick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-754-332

Query Match 100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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DB 1 MDPARPLGLSTILLFLTEALAGDAAQEPYNNABICLLPLDYGPCRAILLRYYDYRYQS 60
QY 61 CROFLYGGCEGNANNTFYWEACDDACRIEYPKYCGLOVSDVDDCEBSTEKTFYFNLSM 120
DB 61 CROFLYGGCEGNANNTFYWEACDDACRIEYPKYCGLOVSDVDDCEBSTEKTFYFNLSM 120
QY 121 TCERFPGSGCHRNRIENRFPDEATCMGFCAPKIPSPFCSPADEGLCSANTYRYENRY 180
DB 121 TCERFPGSGCHRNRIENRFPDEATCMGFCAPKIPSPFCSPADEGLCSANTYRYENRY 180
QY 181 RTCDAPFTYTGCGNDNPFVSRBEDCKRACAKLKKKKKPKLRFPASIRIKRKQF 235
DB 181 RTCDAPFTYTGCGNDNPFVSRBEDCKRACAKLKKKKKPKLRFPASIRIKRKQF 235

RESULT 14
US-09-651-563-332
Sequence 332, Application US/09651563
Patent No. 6914132
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Derrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/651,563
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 1679
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-563-332

Query Match      100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPGLSTLLFLTEALGDAAGPPTGNNAEICLLPLDYGCRALLRYYDRYTQS 60
Db       1 MDPARPGLSTLLFLTEALGDAAGPPTGNNAEICLLPLDYGCRALLRYYDRYTQS 60

QY      61 CROPLVGGCEGNANPYTWEACDDACWRIKVPKCYLQVSVDDQCEGSTYKFFNLSSM 120
Db       61 CROPLVGGCEGNANPYTWEACDDACWRIKVPKCYLQVSVDDQCEGSTYKFFNLSSM 120

QY      121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCYSPKDGCLSANVTRYFNPY 180
Db       121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCYSPKDGCLSANVTRYFNPY 180

QY      181 RTCDAFYYTGGCGNDNNFVSREDCKRACAVALKKKKMPKLRFPASRIRKIKQPF 235
Db       181 RTCDAFYYTGGCGNDNNFVSREDCKRACAVALKKKKMPKLRFPASRIRKIKQPF 235

RESULT 15
US-09-519-642-332
US-09-519-642-332
Sequence 332; Application US/09519642
Patent No. 6933363
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C4
CURRENT APPLICATION NUMBER: US/09/519,642
CURRENT FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 789
SOFTWARE: PaacSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-519-642-332

Query Match      100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPGLSTLLFLTEALGDAAGPPTGNNAEICLLPLDYGCRALLRYYDRYTQS 60
Db       1 MDPARPGLSTLLFLTEALGDAAGPPTGNNAEICLLPLDYGCRALLRYYDRYTQS 60

QY      61 CROPLVGGCEGNANPYTWEACDDACWRIKVPKCYLQVSVDDQCEGSTYKFFNLSSM 120
Db       61 CROPLVGGCEGNANPYTWEACDDACWRIKVPKCYLQVSVDDQCEGSTYKFFNLSSM 120

QY      121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCYSPKDGCLSANVTRYFNPY 180
Db       121 TCCEFFSGGCHRRRIENRFPDEATCMGFCAPKKIPSCYSPKDGCLSANVTRYFNPY 180

QY      181 RTCDAFYYTGGCGNDNNFVSREDCKRACAVALKKKKMPKLRFPASRIRKIKQPF 235
Db       181 RTCDAFYYTGGCGNDNNFVSREDCKRACAVALKKKKMPKLRFPASRIRKIKQPF 235

Search completed: March 9, 2006, 19:58:24
Job time : 48 secs

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Search completed: March 9, 2006, 19:58:24  
Job time : 48 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 20:08:14 ; Search time 165 Seconds  
(without alignments)  
595.090 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPAPPLGSLILFLTEA.....KMPKLRPASRIKIRKKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
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2: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/prodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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5: /cgn2\_6/prodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
6: /cgn2\_6/prodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	3	US-09-904-621-2
2	1306	100.0	235	3	US-09-736-457-332
3	1306	100.0	235	3	US-09-902-941-332
4	1306	100.0	235	3	US-09-849-626-332
5	1306	100.0	235	3	US-09-476-300-332
6	1306	100.0	235	4	US-10-017-754-332
7	1306	100.0	235	4	US-10-060-036-167
8	1306	100.0	235	4	US-10-097-340-316
9	1306	100.0	235	4	US-10-021-660-119
10	1306	100.0	235	4	US-10-113-872-332
11	1306	100.0	235	4	US-10-283-017-332
12	1306	100.0	235	4	US-10-295-027-24
13	1306	100.0	235	4	US-10-428-487-7
14	1306	100.0	235	4	US-10-211-462-52
15	1306	100.0	235	5	US-10-680-684-2
16	1306	100.0	235	5	US-10-800-057-2
17	1306	100.0	235	5	US-10-991-321-24
18	1306	100.0	235	6	US-11-050-926-316
19	1200	91.9	213	4	US-09-766-778-2
20	1200	91.9	213	4	US-10-086-176A-6
21	703.5	53.9	184	4	US-10-425-115-318379
22	464	35.5	88	5	US-09-978-418-26
23	464	35.5	88	5	US-10-485-231-26
24	394.5	30.2	291	3	US-09-992-600A-48
25	394.5	30.2	291	3	US-09-924-340-48
26	394.5	30.2	291	3	US-09-992-095B-48
27	394.5	30.2	291	3	US-09-999-570-48

28	394.5	30.2	291	4	US-10-000-489-48	Sequence 48, App1
29	394.5	30.2	291	4	US-10-000-986-48	Sequence 48, App1
30	394.5	30.2	291	4	US-10-154-678-48	Sequence 48, App1
31	394.5	30.2	291	5	US-10-838-854-48	Sequence 48, App1
32	393.5	30.1	291	3	US-09-992-600A-52	Sequence 52, App1
33	393.5	30.1	291	3	US-09-924-340-52	Sequence 52, App1
34	393.5	30.1	291	3	US-09-992-095B-52	Sequence 52, App1
35	393.5	30.1	291	3	US-09-999-570-52	Sequence 52, App1
36	393.5	30.1	291	4	US-10-000-489-52	Sequence 52, App1
37	393.5	30.1	291	4	US-10-000-986-52	Sequence 52, App1
38	393.5	30.1	291	4	US-10-154-678-52	Sequence 52, App1
39	393.5	30.1	291	5	US-10-838-854-52	Sequence 52, App1
40	388	29.7	304	4	US-10-167-351-1	Sequence 1, App1
41	388	29.7	304	4	US-10-753-544-3	Sequence 412, App
42	388	29.7	304	4	US-10-755-544-3	Sequence 3, App1
43	388	29.7	304	5	US-10-931-153-1	Sequence 1, App1
44	388	29.7	304	5	US-10-367-057-69	Sequence 69, App1
45	388	29.7	304	5	US-10-953-902A-54	Sequence 54, App1

#### ALIGNMENTS

```

RESULT 1
US-09-904-621-2
; Sequence 2, Application US/09904621
; Patent No. US20020098560A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kistler, Walter
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
; TITLE OF INVENTION: AND
; FILE REFERENCE: 93-14D3
; CURRENT APPLICATION NUMBER: US/09/904,621
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-621-2

Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPAPPLGSLILFLTEAALGDAAGPYGNNALICLPLDYGPCRALILRYRYDRTOS 60
DB      1 MDPAPPLGSLILFLTEAALGDAAGPYGNNALICLPLDYGPCRALILRYRYDRTOS 60

QY      61 CQPLFYGGCGNANNFTYWEACDCAWRIEYKPYKICRLQVSYDDQCEGSTEKFFNLSM 120
DB      61 CQPLFYGGCGNANNFTYWEACDCAWRIEYKPYKICRLQVSYDDQCEGSTEKFFNLSM 120

QY      121 TCEKPPSGGCHNRRLENRPDPAATCMGFCAPKKITSFCVSPDEGLCSANVRYFNPRY 180
DB      121 TCEKPPSGGCHNRRLENRPDPAATCMGFCAPKKITSFCVSPDEGLCSANVRYFNPRY 180

QY      181 RTCDAAFTYGGCGANNFVSRBDCKRACAKALKKKKKPKLRFASRIKIRKKQF 235
DB      181 RTCDAAFTYGGCGANNFVSRBDCKRACAKALKKKKKPKLRFASRIKIRKKQF 235

RESULT 2
US-09-736-457-332
; Sequence 332, Application US/09736457

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; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-736-457-332

```

```

Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
QY 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235

```

```

RESULT 3
US-09-902-941-332
; Sequence 332, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnierakis, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

US-09-902-941-332
Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
QY 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235

```

```

RESULT 4
US-09-849-626-332
; Sequence 332, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Liqun
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-849-626-332

```

```

Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
DB 1 MDPARPLGSLILLFLTEAALGDAAGPTGNNABICLLPLDYGPCALLRLYYDRYTS 60
QY 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
DB 61 CROPLYGCGEGNANNFYTWACDDACWRIEKVKYKRLQVSDVDDCGESTETKFFNLSSM 120
QY 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
DB 121 TCEKFFSGGCHRRNIENRFPDEATCMGFCAPKKIIPFCYSPDEGLCSANTVRYFNPRY 180
QY 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235
DB 181 RTCDAPFTYTGCGGNDNNFVSRDCCRACAKALKKKKKMPKLPASIRIRIKRKOP 235

```



```
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaltanya S.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C3
/ CURRENT APPLICATION NUMBER: US/09/476,300
/ CURRENT FILING DATE: 1999-12-30
/ NUMBER OF SEQ ID NOS: 785
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-09-476-300-332

Query Match      100.0%; Score 1306; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
DB 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
QY 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
DB 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
DB 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
```

```
RESULT 6
US-10-017-754-332
/ Sequence 332, Application US/10017754
/ Publication No. US20030054363A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Reiter, Marc W.
/ APPLICANT: Marnerakis, Margarita
/ APPLICANT: Carter, Darick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaltanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.478C18
/ CURRENT APPLICATION NUMBER: US/10/017,754
/ CURRENT FILING DATE: 2001-10-29
/ NUMBER OF SEQ ID NOS: 2004
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-017-754-332
```

```
Query Match      100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
DB 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
```

```
QY 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
DB 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
DB 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
```

```
RESULT 7
US-10-060-036-167
/ Sequence 167, Application US/10060036
/ Publication No. US20030073144A1
/ GENERAL INFORMATION:
/ APPLICANT: Benson, Darin R.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Persing, David H.
/ APPLICANT: Hepler, William T.
/ APPLICANT: Jiang, Yugu
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.566
/ CURRENT APPLICATION NUMBER: US/10/060,036
/ CURRENT FILING DATE: 2002-01-30
/ NUMBER OF SEQ ID NOS: 4560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 167
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-10-060-036-167

Query Match      100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2,6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
DB 1 MDPARPLGSLILFLTEALGDAOEPYGNNAICLLPLDYGPCRALILRYRYDRYTOS 60
QY 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
DB 61 CROFLYGCGEGNANFYTWACDDACMRLEKVPKVCRLQVSVDDOCESGSTEKXFENLSM 120
QY 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
DB 121 TCEKFPSSGCHNRRIENRPPDEATCMGFCAPKKIPSCYSPKDEGLCSANVTRYFNPRY 180
QY 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
DB 181 RTCDATFTYGGCGNNNFVSRDCKRACAKALKKKKKMPKLPASIRIRIRKKOP 235
```

```
RESULT 8
US-10-097-340-316
/ Sequence 316, Application US/10097340
/ Publication No. US20030087250A1
/ GENERAL INFORMATION:
/ APPLICANT: John MONAHAN
/ APPLICANT: Manjula GANNAVAPU
/ APPLICANT: Sebastian HORSCH
/ APPLICANT: Shubhangi KAMATKAR
/ APPLICANT: Steve G. KOVATS
/ APPLICANT: Rachel E. MEYERS
/ APPLICANT: Michael MORRISSEY
/ APPLICANT: Peter OLANDT
/ APPLICANT: Ami SEN
```

```
/ APPLICANT: Peter VEIBY
/ APPLICANT: Gordon B. MILLS
/ APPLICANT: Robert C. BAST, Jr.
/ APPLICANT: Karen LU
/ APPLICANT: Rosemarie SCHMANDT
/ APPLICANT: Xumei ZHAO
/ APPLICANT: Karen GIATT
/ TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
/ FILE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
/ FILE REFERENCE: MRI-030
/ CURRENT APPLICATION NUMBER: US/10/097,340
/ PRIOR FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: 60/276,025
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/325,149
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/276,026
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: 60/324,967
/ PRIOR FILING DATE: 2001/09/26
/ PRIOR APPLICATION NUMBER: 60/311,732
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: 60/325,102
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: 60/323,580
/ PRIOR FILING DATE: 2001-09-19
/ NUMBER OF SEQ ID NOS: 363
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 316
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-097-340-316
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Query Match 100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
DB 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
QY 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
DB 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
QY 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
DB 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235

RESULT 9
US-10-021-660-119
/ Sequence 119, Application US/10021660
/ Publication No. US20030152926A1
/ GENERAL INFORMATION:
/ APPLICANT: Murray, Richard
/ APPLICANT: Glynn, Richard
/ APPLICANT: Watson, Susan R.
/ APPLICANT: EOS Biotechnology, Inc.
/ TITLE OF INVENTION: Compositions and Methods of Diagnosis of Angiogenesis,
/ TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
/ TITLE OF INVENTION: Modulators
/ FILE REFERENCE: 018501-0007100S
/ CURRENT APPLICATION NUMBER: US/10/021,660
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: US/09/784,356
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: US 09/637,977
```

```
/ PRIOR FILING DATE: 2000-08-11
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FaastSeq for Windows Version 3.0
/ SEQ ID NO 119
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-021-660-119
```

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Query Match 100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
DB 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
QY 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
DB 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
QY 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
DB 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235
```

```
RESULT 10
US-10-113-872-332
/ Sequence 332, Application US/10113872
/ Publication No. US20030170255A1
/ GENERAL INFORMATION:
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darick
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C19
/ CURRENT APPLICATION NUMBER: US/10/113,872
/ CURRENT FILING DATE: 2002-03-28
/ NUMBER OF SEQ ID NOS: 2011
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-113-872-332
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```
Query Match 100.0%; Score 1306; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
DB 1 MDPARPLGSLILLFLTEALAGDAQAEPYNNAAICLLPLDYGPCRALLRLYYRYRYS 60
QY 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
DB 61 CRQFLYGGCEGNANFYWEACDDACWRIEKYKVCRLQVSVDDCGESTETKYPFNLSM 120
QY 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
DB 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPDEGLCSANVTRYFNRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKLKKKKMPKLRFASIRIRIKRQK 235
```

Db 181 RTCAFTYTGCGGNDNFVSRBDCRACAKALKKKKKMPKLRPASIRIRIKRQF 235

RESULT 11

US-10-283-017-332

/ Sequence 332, Application US/10283017

/ Publication No. US20030211510A1

/ GENERAL INFORMATION:

/ APPLICANT: Henderson, Robert A.

/ APPLICANT: Wang, Tongrong

/ APPLICANT: Watanabe, Yoshihiro

/ APPLICANT: Kales, Michael D.

/ APPLICANT: Sleath, Paul R.

/ APPLICANT: Johnson, Jeffrey C.

/ APPLICANT: Reiter, Marc W.

/ APPLICANT: Durham, Margalita

/ APPLICANT: Carter, Darick

/ APPLICANT: Panger, Gary R.

/ APPLICANT: Vedvick, Thomas S.

/ APPLICANT: Bangur, Chaitanya S.

/ APPLICANT: McNabb, Andria

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

/ FILE REFERENCE: 210121.478C20

/ CURRENT APPLICATION NUMBER: US/10/283,017

/ CURRENT FILING DATE: 2002-10-28

/ NUMBER OF SEQ ID NOS: 2157

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 332

/ LENGTH: 235

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-283-017-332

Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYDYRYS 60

Db 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYDYRYS 60

Qy 61 CROPFYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Db 61 CROPFYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Qy 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCI PSFCYSPDEGLCSANVTRYFNPRY 180

Db 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCI PSFCYSPDEGLCSANVTRYFNPRY 180

Qy 181 RTCAFTYTGCGGNDNFVSRBDCRACAKALKKKKKMPKLRPASIRIRIKRQF 235

Db 181 RTCAFTYTGCGGNDNFVSRBDCRACAKALKKKKKMPKLRPASIRIRIKRQF 235

RESULT 12

US-10-295-027-24

/ Sequence 24, Application US/10295027

/ Publication No. US20030232350A1

/ GENERAL INFORMATION:

/ APPLICANT: Afar, Daniel

/ APPLICANT: Aziz, Natsaba

/ APPLICANT: Ginsberg, Wendy M.

/ APPLICANT: Gish, Kurt C.

/ APPLICANT: Glynn, Richard

/ APPLICANT: Hevezl, Peter A.

/ APPLICANT: Mack, David H.

/ APPLICANT: Murray, Richard

/ APPLICANT: Watson, Susan R.

/ APPLICANT: Eos Biotechnology, Inc.

/ TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and

/ TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

/ FILE REFERENCE: 018501-012500US

/ CURRENT APPLICATION NUMBER: US/10/295,027

/ CURRENT FILING DATE: 2002-11-13

/ PRIOR APPLICATION NUMBER: US 09/663,733

/ PRIOR FILING DATE: 2000-09-15

/ PRIOR APPLICATION NUMBER: US 60/350,666

/ PRIOR FILING DATE: 2001-11-13

/ PRIOR APPLICATION NUMBER: US 60/335,394

/ PRIOR FILING DATE: 2001-11-15

/ PRIOR APPLICATION NUMBER: US 60/332,464

/ PRIOR FILING DATE: 2001-11-21

/ PRIOR APPLICATION NUMBER: US 60/334,393

/ PRIOR FILING DATE: 2001-11-29

/ PRIOR APPLICATION NUMBER: US 60/340,376

/ PRIOR FILING DATE: 2001-12-14

/ PRIOR APPLICATION NUMBER: US 60/347,211

/ PRIOR FILING DATE: 2002-01-08

/ PRIOR APPLICATION NUMBER: US 60/347,349

/ PRIOR FILING DATE: 2002-01-10

/ PRIOR APPLICATION NUMBER: US 60/355,250

/ PRIOR FILING DATE: 2002-02-08

/ PRIOR APPLICATION NUMBER: US 60/356,714

/ Remaining Prior Application data removed - See file Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 1366

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 24

/ LENGTH: 235

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-295-027-24

Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-116; Mismatches 0; Indels 0; Gaps 0;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYDYRYS 60

Db 1 MDPARPLGSLILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYDYRYS 60

Qy 61 CROPFYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Db 61 CROPFYGCCEGANNFYTWBACDDACWRIEKVPKVCRLQVSDQCEGSTERYFNNLSM 120

Qy 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCI PSFCYSPDEGLCSANVTRYFNPRY 180

Db 121 TCEKFPSSGCHNRLENRPDEATCMGFCAPKCI PSFCYSPDEGLCSANVTRYFNPRY 180

Qy 181 RTCAFTYTGCGGNDNFVSRBDCRACAKALKKKKKMPKLRPASIRIRIKRQF 235

Db 181 RTCAFTYTGCGGNDNFVSRBDCRACAKALKKKKKMPKLRPASIRIRIKRQF 235

RESULT 13

US-10-428-487-7

/ Sequence 7, Application US/10428487

/ Publication No. US20040006780A1

/ GENERAL INFORMATION:

/ APPLICANT: RASTELLI, LUCA K.

/ APPLICANT: GERBER, HANS-PETER

/ TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM

/ FILE REFERENCE: 09800080-0103

/ CURRENT APPLICATION NUMBER: US/10/428,487

/ CURRENT FILING DATE: 2003-05-02

/ PRIOR APPLICATION NUMBER: 09/815,153

/ PRIOR FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: 60/191,201

/ PRIOR FILING DATE: 2000-03-22

/ NUMBER OF SEQ ID NOS: 84

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 7

/ LENGTH: 235

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-428-487-7

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
DB 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
QY 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235  
DB 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235

RESULT 14

US-10-211-462-52  
; Sequence 52, Application US/10211462  
; Publication No. US2004003495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-462-52

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
DB 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
QY 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235  
DB 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235

RESULT 15  
US-10-680-684-2  
; Sequence 2, Application US/10680684  
; Publication No. US20040253686A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Kistel, Walter  
; APPLICANT: Foster, Donald C.  
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
; TITLE OF INVENTION: AND  
; TITLE OF INVENTION: METHODS RELATING THERETO  
; FILE REFERENCE: 93-14D3  
; CURRENT APPLICATION NUMBER: US/10/680,684  
; CURRENT FILING DATE: 2003-10-07  
; PRIOR APPLICATION NUMBER: US/09/904,621  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627  
; PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338  
; PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-680-684-2

Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 2.6e-116;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
DB 1 MDPAPPLGISTILLFLTEALGDAQAEPYNNAAICLPLDYGPCRALLRYYDRYQS 60  
QY 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
DB 61 CRQFLYGGCEGNANFPYWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSM 120  
QY 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
DB 121 TCEKFPSSGCHNRNIENRPPDEATCMGFCAPKKIPSPFCYSPROEGLCSANTTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235  
DB 181 RTCDAFYTYGCGGNDNFPVSRBDCRACAKALKKKKKMPKLPASRIRIKRKQP 235

Search completed: March 9, 2006, 20:11:33  
Job time : 167 secs

GenCore version 5.1.7  
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OM protein - protein search, using SW model

Run on: March 9, 2006, 20:08:54 ; Search time 23 Seconds  
(without alignments)  
284,400 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306  
Sequence: 1 MDPARPLGSLILLFLTEBA.....KMPKLRFPASIRIRIKKQF 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 16167 seqs, 27834885 residues

Total number of hits satisfying chosen parameters: 16167

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- Published Applications AA New:\*
- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB pep:\*
  - 2: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB pep:\*
  - 3: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB pep:\*
  - 4: /cgn2\_6/ptodata/1/pubppa/PCF\_NEW\_PUB pep:\*
  - 5: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB pep:\*
  - 6: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB pep:\*
  - 7: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB pep:\*
  - 8: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	6 US-10-821-234-1398	Sequence 1398, App
2	1200	91.9	213	7 US-11-183-555-6	Sequence 6, App1
3	388	29.7	304	6 US-10-821-234-1540	Sequence 1540, App
4	384.5	29.4	276	7 US-11-183-555-5	Sequence 5, App1
5	180	13.8	352	7 US-11-000-463-450	Sequence 450, App
6	180	13.8	352	7 US-11-000-463-922	Sequence 922, App
7	180	13.8	352	7 US-11-177-506-28	Sequence 28, App1
8	179.5	13.7	548	7 US-11-137-465-47	Sequence 47, App1
9	160	12.3	94	6 US-10-821-234-1123	Sequence 1123, App
10	146	11.2	58	7 US-11-068-783-54	Sequence 54, App1
11	141	10.8	770	6 US-10-982-545-15	Sequence 15, App1
12	141	10.8	770	6 US-10-789-273-38	Sequence 38, App1
13	130	10.0	763	6 US-10-821-234-1619	Sequence 1619, App
14	125	9.6	353	7 US-11-137-465-44	Sequence 44, App1
15	125	9.6	448	7 US-11-137-465-45	Sequence 45, App1
16	124	9.5	99	5 US-09-978-360A-492	Sequence 492, App
17	116	8.9	99	5 US-09-978-360A-618	Sequence 618, App
18	107	8.2	1210	7 US-11-113-202-6	Sequence 6, App1
19	107	8.2	1210	7 US-11-145-566-1	Sequence 1, App1
20	103	7.9	23	7 US-11-183-555-4	Sequence 4, App1
21	97.5	7.5	1308	6 US-10-912-971-12	Sequence 12, App1
22	97.5	7.5	1308	6 US-11-113-202-16	Sequence 16, App1
23	90	6.9	317	6 US-10-620-787-21	Sequence 21, App1
24	88	6.7	317	6 US-10-620-787-22	Sequence 22, App1
25	88	6.7	963	6 US-10-995-561-923	Sequence 923, App

26	88	6.7	963	6 US-10-453-372-660	Sequence 660, App
27	88	6.7	1012	6 US-10-453-372-646	Sequence 646, App
28	87	6.7	3333	6 US-10-766-317-4	Sequence 4, App1
29	86.5	6.6	3597	7 US-11-019-711-6	Sequence 6, App1
30	86.5	6.6	3600	7 US-11-019-711-2	Sequence 2, App1
31	86	6.6	1001	7 US-11-132-285-40	Sequence 40, App1
32	86	6.6	1013	6 US-10-131-826A-38	Sequence 38, App1
33	86	6.6	1013	6 US-10-973-115B-38	Sequence 38, App1
34	85.5	6.5	707	7 US-11-072-517-3162	Sequence 3162, App
35	83.5	6.4	3714	6 US-10-995-561-1015	Sequence 1015, App
36	83.5	6.4	3717	6 US-10-821-234-1076	Sequence 1076, App
37	82	6.3	4544	6 US-10-501-035-214	Sequence 214, App1
38	82	6.3	4544	7 US-11-076-427A-32	Sequence 32, App1
39	81	6.2	340	7 US-11-226-657-174	Sequence 174, App
40	80.5	6.2	2923	7 US-11-200-822-3	Sequence 3, App1
41	79	6.0	243	6 US-10-512-109-23	Sequence 23, App1
42	79	6.0	721	7 US-11-022-478-12	Sequence 12, App1
43	78	6.0	1620	6 US-10-055-877-213	Sequence 213, App
44	78	6.0	1664	6 US-10-055-877-212	Sequence 212, App
45	77.5	5.9	365	7 US-11-108-528-56	Sequence 56, App1

## ALIGNMENTS

```

RESULT 1
US-10-821-234-1398
; Sequence 1398, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andamiani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Method for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCES: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc SEQ_genes Version 1.0
; SEQ ID NO 1398
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1398

Query Match      100.0% Score 1306; DB 6; Length 235;
Best Local Similarity 100.0% Pred. No. 3.7e-122;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDPARPLGSLILLFLTEBALGDAQEPYNNABICLPLDYGPCRALILRYDRYTQS 60
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DB      1 MDPARPLGSLILLFLTEBALGDAQEPYNNABICLPLDYGPCRALILRYDRYTQS 60
      |||
QY      61 CROPLTYGCGEANNFTYTBACDCAKRIKPKVCRLOVSVDDQCEGSTEKFFNLSM 120
      |||
DB      61 CROPLTYGCGEANNFTYTBACDCAKRIKPKVCRLOVSVDDQCEGSTEKFFNLSM 120
      |||
QY      121 TCCKFPSSGCHNRIRNRPDEATCMGFCAPKKIPSEFCSPDEGLCSANVRYFNPRY 180
      |||
DB      121 TCCKFPSSGCHNRIRNRPDEATCMGFCAPKKIPSEFCSPDEGLCSANVRYFNPRY 180
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QY      181 RTCDATYTYGCGGNDNNFVSRBDCRKAQKAKLKKKKMFKLFPASIRIRIKKQF 235
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DB      181 RTCDATYTYGCGGNDNNFVSRBDCRKAQKAKLKKKKMFKLFPASIRIRIKKQF 235
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RESULT 2
US-11-183-555-6
; Sequence 6, Application US/11183555
; Publication No. US20060025329A1
  
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GENERAL INFORMATION:  
APPLICANT: Hembrough, Todd  
APPLICANT: Papachanasidu, Adonia E.  
APPLICANT: Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation  
TITLE OF INVENTION: Compositing TPEI Fragments  
FILE REFERENCE: 05213-0297 (43170-300210)  
CURRENT APPLICATION NUMBER: US/11/183,555  
PRIOR FILING DATE: 2005-07-18  
PRIOR APPLICATION NUMBER: US 09/766,778  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/227,955  
PRIOR FILING DATE: 1999-01-11  
PRIOR APPLICATION NUMBER: US 08/796,850  
PRIOR FILING DATE: 1997-02-06  
PRIOR APPLICATION NUMBER: US 09/130,273  
PRIOR FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 6  
LENGTH: 213  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-11-183-555-6

Query Match 91.9%; Score 1200; DB 7; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1,1e-111; Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAQPTGNNAAICLLPDDYPCRALLLRYYDRYQSCROPLVYSGCEGNANFYTWAC 82  
DB 1 DAAQPTGNNAAICLLPDDYPCRALLLRYYDRYQSCROPLVYSGCEGNANFYTWAC 60  
QY 83 DDAQPTGNNAAICLLPDDYPCRALLLRYYDRYQSCROPLVYSGCEGNANFYTWAC 142  
DB 61 DDAQPTGNNAAICLLPDDYPCRALLLRYYDRYQSCROPLVYSGCEGNANFYTWAC 120  
QY 143 ATCMGFCAPKIPKICRQVSVDDCEGSTEKYPNLSMTCEKFPSCGCHRNRIENRFPDB 202  
DB 121 ATCMGFCAPKIPKICRQVSVDDCEGSTEKYPNLSMTCEKFPSCGCHRNRIENRFPDB 180  
QY 203 DCKRACAKALKKKKKPKLRPAIRIRIRKKOP 235  
DB 181 DCKRACAKALKKKKKPKLRPAIRIRIRKKOP 213

RESULT 3  
US-10-821-234-1540  
Sequence 1540, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmani, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
PRIOR FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt SEQ\_genes Version 1.0  
SEQ ID NO 1540  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1540

Query Match 29.7%; Score 388; DB 6; Length 304;  
Best Local Similarity 30.3%; Pred. No. 4.3e-31;

Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8;  
QY 12 LLLPTEALGDAQOE-----PTGNNAEICLLPDDYPCRALLLRYYDRYT 58  
DB 17 LLLNPAPALNDSEDEHHTITTELPPLKLMSFCAFKADDGCKAIMRFFNIFT 76  
QY 59 QGCRQPLVYSGCEGNANFYTWACDCAWR-----IEKVPKICRLQVSDQ-- 105  
DB 77 ROCBEIYVGCCEGNQGRFSLBECKKMCYRDANRRIKTTLOEKBDPFCFL--BDPGI 133  
QY 106 CGSTEKYPNLSMTCEKFPSCGCHRNRIENRFPDEATCMGFC----- 149  
DB 134 CGGYITRYPNNQTCERFKYGGCLGNM--NNFTLBECKNICBDPNGPOVDNYGTOL 191  
QY 150 -----APKXI-----PSFCYSPKDEGLCSANTRYFNPRTCDAFYTGCG 192  
DB 192 NAVNNSLTPOSTKIVBSLPEFHGPSWCLTPADGLCRANNNRYYNSVIGKCPFKISGCG 251  
QY 193 GNDNNFVSRDECKRACAKAL-----KCKKMPKLRPA 224  
DB 252 GNENNFTSKQECILRACKGFIQISKGLIKTKRRKKQKVXIA 295

RESULT 4  
US-11-183-555-5  
Sequence 5, Application US/1183555  
Publication No. US20060025329A1  
GENERAL INFORMATION:  
APPLICANT: Hembrough, Todd  
APPLICANT: Papachanasidu, Adonia E.  
APPLICANT: Green, Shawn J.  
TITLE OF INVENTION: Compositions and Methods for Inhibiting Cellular Proliferation  
TITLE OF INVENTION: Compositing TPEI Fragments  
FILE REFERENCE: 05213-0297 (43170-300210)  
CURRENT APPLICATION NUMBER: US/11/183,555  
PRIOR FILING DATE: 2005-07-18  
PRIOR APPLICATION NUMBER: US 09/766,778  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/227,955  
PRIOR FILING DATE: 1999-01-11  
PRIOR APPLICATION NUMBER: US 08/796,850  
PRIOR FILING DATE: 1997-02-06  
PRIOR APPLICATION NUMBER: US 09/130,273  
PRIOR FILING DATE: 1998-08-06  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide  
US-11-183-555-5

Query Match 29.4%; Score 384.5; DB 7; Length 276;  
Best Local Similarity 31.6%; Pred. No. 8.6e-31;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLLPDDYPCRALLLRYYDRYQSCROPLVYSGCEGNANFYTWACDCAWR----- 88  
DB 26 CAFPADDGCKAIMRFFNIFTROCBERTYVGCCEGNQGRFSLBECKKMCYRDANRRI 85  
QY 89 -----IEKVPKICRLQVSDQ--CEGSTEKYPNLSMTCEKFPSCGCHRNRIENRFPDB 142  
DB 86 KTTLOEKBDPFCFL--EDBGICGYITRYPNNQTCERFKYGGCLGNM--NNFTL 140  
QY 143 ATCMGFC-----APKXI-----PSFCYSPKDEGLCSA 169  
DB 141 BECKNICBDPNGPOVDNYGTOLAVNNSLTPOSTKIVBSLPEFHGPSWCLTPADGLCSA 200  
QY 170 NTRITRYPNRTCDAFYTGCGGNDNNFVSRDECKRACAKAL-----KCKK 217  
DB 201 NENRYYNSVIGKCPFKISGCGGNENNFTSKQECILRACKGFIQISKGLIKTKRRKK 260

QY 218 MPKLRRA 224  
DB 261 KORVKIA 267

## RESULT 5

US-11-000-463-450  
Sequence 450, Application US/11000463  
Publication No. US2005026423A1  
GENERAL INFORMATION:

APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
APPLICANT: Dramnac, Radolje T.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIP4CN

CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 450  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-000-463-450

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVCRLOVSVDDQEGSTERYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
DB 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKELQ 280  
QY 149 CAPKIPSCFYSPKDGCLGSANVTTRYFNPRTCDAPFTYTCGGGNDNNFVSRDECKRAC 208  
DB 281 C---RTVAACNLPYVGPGRARFQIOWAFDVAVKGCYVLPFYGGCGGNGNKFYSKECKREYC 337

## RESULT 6

US-11-000-463-922  
Sequence 922, Application US/11000463  
Publication No. US2005026423A1  
GENERAL INFORMATION:

APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Chen, Rui-hong  
APPLICANT: Qian, Xiaohong B.  
APPLICANT: Wang, Zhiwei  
APPLICANT: Wehrman, Tom

APPLICANT: Zhang, Jie  
APPLICANT: Zhou, Ping  
APPLICANT: Cao, Yi-Cheng  
APPLICANT: Dramnac, Radolje T.  
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
FILE REFERENCE: 785CIP4CN

CURRENT APPLICATION NUMBER: US/11/000,463  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: 10/291,265  
PRIOR FILING DATE: 2002-11-08  
PRIOR APPLICATION NUMBER: PCT/US01/02623  
PRIOR FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: 09/922,279  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: 09/491,404  
PRIOR FILING DATE: 2000-01-25  
PRIOR APPLICATION NUMBER: 09/617,746  
PRIOR FILING DATE: 2000-07-17  
PRIOR APPLICATION NUMBER: 09/631,451  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: 09/633,870  
PRIOR FILING DATE: 2000-09-15  
NUMBER OF SEQ ID NOS: 944  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 922  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-000-463-922

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVCRLOVSVDDQEGSTERYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
DB 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKELQ 280  
QY 149 CAPKIPSCFYSPKDGCLGSANVTTRYFNPRTCDAPFTYTCGGGNDNNFVSRDECKRAC 208  
DB 281 C---RTVAACNLPYVGPGRARFQIOWAFDVAVKGCYVLPFYGGCGGNGNKFYSKECKREYC 337

## RESULT 7

US-11-177-506-28  
Sequence 28, Application US/11177506  
Publication No. US20060029956A1  
GENERAL INFORMATION:

APPLICANT: Beyer, Wayne F.  
APPLICANT: Groelke, John W.  
APPLICANT: Blasius, Rainer H.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE  
DETECTION OF OVARIAN DISEASE  
FILE REFERENCE: 46143/294851

CURRENT APPLICATION NUMBER: US/11/177,506  
CURRENT FILING DATE: 2005-07-08  
PRIOR APPLICATION NUMBER: 60/586,856  
PRIOR FILING DATE: 2004-07-09  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 28  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-177-506-28

Query Match 13.8%; Score 180; DB 7; Length 352;  
Best Local Similarity 35.0%; Pred. No. 2e-10;  
Matches 42; Conservative 14; Mismatches 58; Indels 6; Gaps 3;

QY 89 IEKPVCRLOVSVDDQEGSTERYFNLSMTCKEFGGCHRRNIENRFPDEATCMGF 148  
DB 224 VTKEDSCQLGYSA-GPCMGMTSRFYNGTSMACEFYGGCGMGN--GNNFVTEKELQ 280  
QY 149 CAPKIPSCFYSPKDGCLGSANVTTRYFNPRTCDAPFTYTCGGGNDNNFVSRDECKRAC 208  
DB 281 C---RTVAACNLPYVGPGRARFQIOWAFDVAVKGCYVLPFYGGCGGNGNKFYSKECKREYC 337



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Db      224 VTKEDSCQGYSA-GEPCMGTSRYFYNGTSMACETFOYGCGNGN--GNNFVTEKCLQT 280
Qy      149 CAPKIPSPFCYSPKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRAC 208
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      281 C---KRVAAQNLPIVAGPCAPFIQLWAFDAVAKKCVLPFGGCGGNGNKFYSKREGRYC 337

RESULT 8
US-11-137-465-47
; Sequence 47, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kadnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-47

Query Match      13.7%; Score 179.5; DB 7; Length 548;
Best Local Similarity 32.8%; Pred. No. 3.6e-10;
Matches 45; Conservative 21; Mismatches 64; Indels 7; Gaps 3;

Qy      18 EALGDAAOEPTGNNAICLLPDIYGRYTGSCROQLYGGCGGNNANFY 77
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Db      345 EACQACARBP---GDACVLPVAVGSPCKGMEPRMAYSPILQCHFPYVGGCGGNNANFY 400

Qy      78 TWEACDCAKRIKVP--KYCRLQVSVDDQCEGSTEREFNLSMTCEKFPSSGCHRNRI 135
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      401 SRSCESDAC-PVPRTPPCRCRLRSKLALSLCRSDPAIVGRLTEVLEPEPAAGIARVAL 459

Qy      136 ENRFPPEATCMGFCAPK 152
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      460 EDVLKDDKRWGLKFLGTR 476

RESULT 9
US-10-821-234-1123
; Sequence 1123, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crahn, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
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; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1123
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1123

Query Match      12.3%; Score 160; DB 6; Length 94;
Best Local Similarity 43.9%; Pred. No. 5e-09;
Matches 25; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy      158 CTSFKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRACAKALXK 214
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      29 CTKLPKDEGTGRDPIFKMYDPTKSCARFMYGCGGNGENKFGSQKCEHYCAVPLAK 85

RESULT 10
US-11-068-783-54
; Sequence 54, Application US/11068783
; Publication No. US20050260715A1
; GENERAL INFORMATION:
; APPLICANT: Burian, Jan
; APPLICANT: Bartfeld, Daniel
; TITLE OF INVENTION: EFFICIENT METHODS FOR PRODUCING
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES IN HOST CELLS
; FILE REFERENCE: 660081.411
; CURRENT APPLICATION NUMBER: US/11/068,783
; PRIOR FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/09/444,281
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-068-783-54

Query Match      11.2%; Score 146; DB 7; Length 58;
Best Local Similarity 43.9%; Pred. No. 7.5e-08;
Matches 25; Conservative 4; Mismatches 28; Indels 0; Gaps 0;

Qy      155 PSFCYSPKDEGLCSANVTRYFNPRYRTCDAFYTYGCGGNDNNFVSREDCKRACAKA 211
        | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 PFCLEPFPYTGCKAIRIRFYNAKALGCTFTVYGGCGKRRNNFSAEDCKMTCGGA 58

RESULT 11
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonson, Anja Hvild
; APPLICANT: Blennow, Kaj
; APPLICANT: Podusz, Vladimir
; APPLICANT: Ciberger Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; PRIOR FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
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PRIOR FILING DATE: 2004-05-18  
PRIOR APPLICATION NUMBER: US 60/586,503  
PRIOR FILING DATE: 2004-07-08  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABP), isoform a, protease  
OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),  
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,  
OTHER INFORMATION: Alzheimer's disease amyloid protein  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)..(17)  
OTHER INFORMATION: signal peptide  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(40)  
OTHER INFORMATION: biomarker peptide 4320 Da (IMC-NI), A-beta 1-40  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (18)..(671)  
OTHER INFORMATION: soluble APP-alpha  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (672)..(713)  
OTHER INFORMATION: beta-amyloid protein 42  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (672)..(711)  
OTHER INFORMATION: biomarker peptide 4320 Da, fragment of Amyloid  
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(770)  
OTHER INFORMATION: C83  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(713)  
OTHER INFORMATION: P3(42)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (688)..(711)  
OTHER INFORMATION: P3(40)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (712)..(770)  
OTHER INFORMATION: gamma-CTF(59)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (714)..(770)  
OTHER INFORMATION: gamma-CTF(57)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (721)..(770)  
OTHER INFORMATION: gamma-CTF(50)  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (740)..(770)  
OTHER INFORMATION: C31  
US-10-982-545-15

Query Match 10.8%; Score 141; DB 6; Length 770;  
Best Local Similarity 47.2%; Pred. No. 3.3e-06;  
Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
Db 289 EVCSBAETGPCRAMISRWYFDVBGKCAPFFYGGCGRRNNDTEYCAVC 341  
34 EICLPLDYGPCRALIARYYDRYTSCHQFLYGGCGGNANFYTWACDDAC 86  
US-10-789-273-38  
Sequence 38, Application US/10789273  
Publication No. US20050249725A1  
GENERAL INFORMATION:  
APPLICANT: Baei, Gurliq  
APPLICANT: Saldanha, Jose  
APPLICANT: Yednock, Ted  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/789,273  
PRIOR FILING DATE: 2004-02-27  
PRIOR APPLICATION NUMBER: US/10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 770  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-789-273-38  
Query Match 10.8%; Score 141; DB 6; Length 770;  
Best Local Similarity 47.2%; Pred. No. 3.3e-06;  
Matches 25; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
Db 289 EVCSBAETGPCRAMISRWYFDVBGKCAPFFYGGCGRRNNDTEYCAVC 341  
34 EICLPLDYGPCRALIARYYDRYTSCHQFLYGGCGGNANFYTWACDDAC 86  
US-10-821-234-1619  
Sequence 1619, Application US/10821234  
Publication No. US20050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmant, Susan  
APPLICANT: Tang, Y. Tom  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
PRIOR FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: PC\_SEQ\_genes Version 1.0  
SEQ ID NO 1619  
LENGTH: 763  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-821-234-1619  
Query Match 10.0%; Score 130; DB 6; Length 763;  
Best Local Similarity 28.6%; Pred. No. 4e-05;  
Matches 34; Conservative 17; Mismatches 48; Indels 20; Gaps 3;



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:57:44 ; Search time 566 Seconds

(without alignments)  
573.780 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPAPRLGSLILFLTEAA.....KKPKRLFPASIRIKRKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	1	PCT-US02-02781-167
2	1306	100.0	235	1	PCT-US02-04915-52
3	1306	100.0	235	1	PCT-US02-07826-116
4	1306	100.0	235	1	PCT-US02-34777-332
5	1306	100.0	235	1	PCT-US94-12609-2
6	1306	100.0	235	18	US-08-800-483-4
7	1306	100.0	235	22	US-09-265-627-2
8	1306	100.0	235	23	US-09-308-853-4
9	1306	100.0	235	24	US-09-466-867-332
10	1306	100.0	235	24	US-09-476-300-332
11	1306	100.0	235	25	US-09-533-077-332
12	1306	100.0	235	25	US-09-546-229-332
13	1306	100.0	235	25	US-09-560-406-332
14	1306	100.0	235	26	US-09-677-419A-332
15	1306	100.0	235	27	US-09-760-443-1224
16	1306	100.0	235	27	US-09-760-447-41
17	1306	100.0	235	27	US-09-784-356-119
18	1306	100.0	235	27	US-09-791-537-96446
19	1306	100.0	235	28	US-09-849-626-332
20	1306	100.0	235	29	US-09-902-941-332
21	1306	100.0	235	30	US-10-021-660-119
22	1306	100.0	235	30	US-10-060-036-167
23	1306	100.0	235	30	US-10-097-340-316
24	1306	100.0	235	31	US-10-113-872-332
25	1306	100.0	235	31	US-10-126-052A-397
26	1306	100.0	235	31	US-10-130-138B-202
27	1306	100.0	235	31	US-10-137-441-41
28	1306	100.0	235	31	US-10-170-205E-764
29	1306	100.0	235	32	US-10-211-462-52
30	1306	100.0	235	32	US-10-212-054-1224
31	1306	100.0	235	32	US-10-283-017-332
32	1306	100.0	235	32	US-10-295-027-24
33	1306	100.0	235	34	US-10-405-027-3268
34	1306	100.0	235	34	US-10-428-467-7
35	1306	100.0	235	36	US-10-680-684-2
36	1306	100.0	235	36	US-10-800-057-2
37	1306	100.0	235	38	US-10-821-234-1398
38	1306	100.0	235	38	US-10-821-801-886
39	1306	100.0	235	39	US-10-940-774A-6735
40	1306	100.0	235	39	US-10-940-774A-6735
41	1306	100.0	235	39	US-10-991-321-24
42	1306	100.0	235	40	US-11-050-926-316
43	1306	100.0	235	48	US-60-406-385-190
44	1306	100.0	235	48	US-60-453-050-11171
45	1306	100.0	235	48	US-60-453-135-11171

#### ALIGNMENTS

RESULT 1  
PCT-US02-02781-167  
; Sequence 167, Application PC/TUS0202781  
; GENERAL INFORMATION:  
; APPLICANT: Corixa Corporation

APPLICANT: Benson, Darin R.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Persing, David H.  
APPLICANT: Hepler, William T.  
APPLICANT: Jiang, Yugu  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.566PC  
CURRENT APPLICATION NUMBER: PCT/US02/02781  
CURRENT FILING DATE: 2002-01-30  
NUMBER OF SEQ ID NOS: 4560  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 167  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-02781-167

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
QY 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
DB 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235

RESULT 2  
PCT-US02-04915-52  
Sequence 52, Application PC/TUS0204915  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glynn, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Aziz, Natsaba  
APPLICANT: Eos Biotechnology, Inc.  
TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
FILE REFERENCE: 018501-006200PC  
CURRENT APPLICATION NUMBER: PCT/US02/04915  
CURRENT FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 09/784,356  
PRIOR FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: US 09/791,390  
PRIOR FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: US 60/285,475  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: US 60/310,025  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 60/350,666  
PRIOR FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: US 60/334,244  
PRIOR FILING DATE: 2001-11-29  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 52  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-04915-52

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
QY 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
DB 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235

RESULT 3  
PCT-US02-07826-316  
Sequence 316, Application PC/TUS0207826  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc. et al.  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
FILE REFERENCE: MRI-030PC  
CURRENT APPLICATION NUMBER: PCT/US02/07826  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 60/276,025  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/325,149  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: 60/276,026  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 60/324,967  
PRIOR FILING DATE: 2001/09/26  
PRIOR APPLICATION NUMBER: 60/311,732  
PRIOR FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: 60/325,102  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 60/323,580  
PRIOR FILING DATE: 2001-09-19  
NUMBER OF SEQ ID NOS: 363  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 316  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-07826-316

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7.7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPFGNNAEICLLPLDYGPCRALILRYRYRYTOS 60  
QY 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
DB 61 CROFLYGGCEGNANFYWEACDDACMRLEKVPKVCRLQVSDDOCEGSTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSPCYSPDDEGLCSANVTRYFNPRY 180  
QY 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235  
DB 181 RTCDAFYTYGCGGNDNNFVSREDCKRAKAKLKKKKMPKJLPFASIRIRIKRKQF 235

RESULT 4  
PCT-US02-34777-332  
Sequence 332, Application PC/TUS0234777  
GENERAL INFORMATION:  
APPLICANT: Corixa Corporation  
APPLICANT: Henderson, Robert A.  
APPLICANT: Wang, Tonglong  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Kalos, Michael D.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Johnson, Jeffrey C.  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margalita  
APPLICANT: Carter, Darick  
APPLICANT: Panger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.47803PC  
CURRENT APPLICATION NUMBER: PCT/US02/34777  
CURRENT FILING DATE: 2002-10-28  
NUMBER OF SEQ ID NOS: 2157  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-34777-332

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7,7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGISILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYTYRYS 60  
DB 1 MDPAPPLGISILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYTYRYS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDEGLCSANTRYTFNRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDEGLCSANTRYTFNRY 180  
QY 181 RTCDAFYTYGGGNDNNFVSRBDCRACAKALKKKKKMPKLRFPASIRIRIRKQF 235  
DB 181 RTCDAFYTYGGGNDNNFVSRBDCRACAKALKKKKKMPKLRFPASIRIRIRKQF 235

RESULT 5  
PCT-US94-12609-2  
Sequence 2, Application PC/TUS9412609  
GENERAL INFORMATION:  
APPLICANT: ZymoGenetics, Inc.  
APPLICANT: 1201 Baseline Avenue East  
APPLICANT: Seattle  
APPLICANT: WA  
APPLICANT: US  
APPLICANT: 98102  
APPLICANT: Scholtes Hall 102  
APPLICANT: Albuquerque  
APPLICANT: NM  
APPLICANT: US  
APPLICANT: 87131  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
TITLE OF INVENTION: METHODS RELATING THERETO  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:

ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Baseline Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/12609  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E.  
REGISTRATION NUMBER: 31-648  
REFERENCE/DOCKET NUMBER: 93-14PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-12609-2

Query Match 100.0%; Score 1306; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 7,7e-138;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGISILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYTYRYS 60  
DB 1 MDPAPPLGISILLFLTEALGDAAQEPYNNABICLLPLDYGPCRALILRYTYRYS 60  
QY 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
DB 61 CRQFLYGGCEGNANFYTWACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKTFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDEGLCSANTRYTFNRY 180  
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKKIPSCYSPDEGLCSANTRYTFNRY 180  
QY 181 RTCDAFYTYGGGNDNNFVSRBDCRACAKALKKKKKMPKLRFPASIRIRIRKQF 235  
DB 181 RTCDAFYTYGGGNDNNFVSRBDCRACAKALKKKKKMPKLRFPASIRIRIRKQF 235

RESULT 6  
US-08-800-483-4  
Sequence 4, Application US/08800483  
GENERAL INFORMATION:  
APPLICANT: Rao, Chilkur N.  
APPLICANT: Woodley, David T.  
TITLE OF INVENTION: USBS OF SERINE PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Rose P. C.  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,483





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QY 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
| | | | |
DB 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
| | | | |
DB 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
| | | | |
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235
| | | | |
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235

RESULT 10
US-09-476-300-332
; Sequence 332, Application US/09476300
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C3
; CURRENT APPLICATION NUMBER: US/09/476,300
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-476-300-332

Query Match 100.0%; Score 1306; DB 24; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
| | | | |
DB 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
| | | | |
DB 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
| | | | |
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235
| | | | |
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235

RESULT 11
US-09-533-077-332
; Sequence 332, Application US/09533077
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C5
; CURRENT APPLICATION NUMBER: US/09/533,077
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 800
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
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; LENGTH: 235
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-533-077-332

Query Match 100.0%; Score 1306; DB 25; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
| | | | |
DB 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
| | | | |
DB 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
| | | | |
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235
| | | | |
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235

RESULT 12
US-09-546-259-332
; Sequence 332, Application US/09546259
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C6
; CURRENT APPLICATION NUMBER: US/09/546,259
; CURRENT FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 803
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-546-259-332

Query Match 100.0%; Score 1306; DB 25; Length 235;
Best Local Similarity 100.0%; Pred. No. 7,7e-138;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
| | | | |
DB 1 MDPARPLGISILLFLTEBALGDAOEPYNNNAEICLLPLDYGPCRALILRYYYDRYTOS 60
QY 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
| | | | |
DB 61 CROFLYGGCEGNANFYTYEACDCAWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLSSM 120
QY 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
| | | | |
DB 121 TCEKPFSSGCHNRRIENRPPDEATCMGFCAPKKIISFCYSPDDEGLCSANVTTRYFNPRY 180
QY 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235
| | | | |
DB 181 RTCDAFYTYGCGGNDNPFVSRDECKRACAKALKKKKKMPKLPASRIRIKRKQF 235

RESULT 13
US-09-560-406-332
; Sequence 332, Application US/09560406
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
```

```

1  APPLICANT: Bangur, Chaitanya S.
2  APPLICANT: Lodes, Michael A.
3  APPLICANT: Fanger, Gary
4  APPLICANT: Vedvick, Tom
5  APPLICANT: Carter, Darriick
6  APPLICANT: Retter, Marc
7  APPLICANT: Mammion, Jane
8  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
9  TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
10 FILE REFERENCE: 210121.478C7
11 CURRENT APPLICATION NUMBER: US/09/560,406
12 CURRENT FILING DATE: 2000-04-27
13 NUMBER OF SEQ ID NOS: 824
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 332
16 LENGTH: 235
17 TYPE: PR1
18 ORGANISM: Homo sapiens
19 US-09-560-406-332

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	Query Match	100.0%;	Score 1306;	DB 25;	Length 235;
	Best Local Similarity	100.0%;	Pred. No. 7'e-138;		
	Matches	235;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MDPARRPGLSTLLPLTEALGDAAOEPTGNNAIRICILPLDYGPCRALLLRYYYDRYTQS	60		
Db	1	MDPARRPGLSTLLPLTEALGDAAOEPTGNNAIRICILPLDYGPCRALLLRYYYDRYTQS	60		
Qy	61	CROPITYGGCEBNANPFTYEAACDCAWRIEAVPYKCRLOVSDVDCBEGSTETKYPFNLSM	120		
Db	61	CROPITYGGCEBNANPFTYEAACDCAWRIEAVPYKCRLOVSDVDCBEGSTETKYPFNLSM	120		
Qy	121	TCEAFPSGGGCHRNRIENRFPDEATCMGFCADPKIIPSFICYSPKDGILGSANTRYYYENRY	180		
Db	121	TCEAFPSGGGCHRNRIENRFPDEATCMGFCADPKIIPSFICYSPKDGILGSANTRYYYENRY	180		
Qy	181	RTCDAPFYTYGCGGNDNPFVSREDCKRACAKALXXXXXMPKLRPSFARTRIKRHKQP	235		
Db	181	RTCDAPFYTYGCGGNDNPFVSREDCKRACAKALXXXXXMPKLRPSFARTRIKRHKQP	235		

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RESULT 14
US-09-677-419A-332
/ Sequence 332, Application US/09677419A
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaltanya S.
/ APPLICANT: Lodes, Michael S.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darick
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Mannion, Jane
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C13
/ CURRENT APPLICATION NUMBER: US/09/677,419A
/ CURRENT FILING DATE: 2000-10-06
/ NUMBER OF SEQ ID NOS: 1825
/ SOFTWARE: PaetSeq for Windows Version 3.0
/ SEQ ID NO 332
/ LENGTH: 235
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-677-419A-332

```

```

Query Match      100.0%; Score 1306; DB 26; Length 235;
Best Local Similarity 100.0%; PId. No. 7, 7e-138;
Matches 235; Conservative 0; Indels 0; Gaps 0;

1 MDAPRLGISTLLFLTEALAGDAOETGNNALICLLPIIDVGCAGALLRRYYDRRYNS 60
|||||

```

Db	1	MDPARPLGSLILLFLTEALGDAQBPYGNNAICILLPLDYGCRALLRLYYDYDRYTG	60
Qy	61	CRQFLYGGEGGNANFYTWACDDA <del>CH</del> IKYIPYCYRLQUSVVDQCGSTETKTFPNTSSM	120
Db	61	CRQFLYGGEGGNANFYTWACDDA <del>CM</del> IKYIPYCYRLQUSVVDQCGSTETKTFPNTSSM	120
Qy	121	TCGKFPSSGGCHNRIENRPPDEATCMGRCAPIKIPSPCYSPKDSGLCSANVTRYENPRY	180
Db	121	TCGKFPSSGGCHNRIENRPPDEATCMGRCAPIKIPSPCYSPKDSGLCSANVTRYENPRY	180
Qy	181	RTCDATFYTGCGGNNNFVSREDCKRA <del>CA</del> KALKKKCKMFKLRFASRI <del>RI</del> KTQF	235
Db	181	RTCDATFYTGCGGNNNFVSREDCKRA <del>CA</del> KALKKKCKMFKLRFASRI <del>RI</del> KTQF	235

```

US-09-760-443-1224
RESULT 15
US-09-760-443-1224
; Sequence 1224, Application US/09760443
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ12
; CURRENT APPLICATION NUMBER: US/09/760,443
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2164
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1224
; LENGTH: 235
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-760-443-1224

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	Query Match	100.0%;	Score 1306;	DB 28;	Length 235;
	Best Local Similarity	100.0%;	Pred. No. 7, 7e-138;		
	Matches 235;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MDPARPLGISLILLFLTEALGDAOEPFGNNARI	CLLPLDYGFCRALLRYYDRTYQS	60	
Db	1	MDPARPLGISLILLFLTEALGDAOEPFGNNARI	CLLPLDYGFCRALLRYYDRTYQS	60	
QY	61	CROFLYGGCEGNANNFYWEACDCAKRIKVPVYCLQYVSVDQCGSTEKYPFNSSM	120		
Db	61	CROPLVGGCEGNANNYYTWACDCAKRIKVPVYCLQYVSVDQCGSTEKYPFNSSM	120		
QY	121	TCSEKFPSSGGCHRRRIENRFPDEATCMGFCAPKCI	PSFCYSPKDEGLCSANTRYRYFNRY	180	
Db	121	TCSEKFPSSGGCHRRRIENRFPDEATCMGFCAPKCI	PSFCYSPKDEGLCSANTRYRYFNRY	180	
QY	181	RTCDATFTYGGCGGNDNNFVSRBECCKACAAUL	KKKKKMPCLRAPSRIRKIRKKQF	235	
Db	181	RTCDATFTYGGCGGNDNNFVSRBECCKACAAUL	KKKKKMPCLRAPSRIRKIRKKQF	235	

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Job time : 568 secs

Search completed: March 9, 2006, 20:07:58  
Job time : 568 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 9, 2006, 19:58:39 ; Search time 39 seconds

(without alignments)  
478.910 Million cell updates/sec

Title: US-10-800-057-2

Perfect score: 1306

Sequence: 1 MDPAPPLGSLILFLTEA.....KMPKLRPASRIKRIKQF 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 339805 seqs, 79478670 residues

Total number of hits satisfying chosen parameters: 339805

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:\*  
1: /cgn2\_6/prodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/paa/US10\_NEW\_COMB.pep:\*  
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8: /cgn2\_6/prodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	US-11-301-554-332	Sequence 332, App
2	1200	91.9	213	US-11-107-643-1	Sequence 1, App1
3	421	32.2	73	US-11-107-643-2	Sequence 2, App1
4	418	32.0	73	US-11-107-643-3	Sequence 3, App1
5	388	29.7	304	PCT-US05-42298-1	Sequence 1, App1
6	388	29.7	304	PCT-US05-34335-54	Sequence 54, App1
7	388	29.4	304	US-11-287-121A-1	Sequence 1, App1
8	384.5	29.4	276	US-11-302-208-1	Sequence 1, App1
9	384.5	29.4	276	US-11-337-518-1	Sequence 1, App1
10	343	26.3	58	PCT-US05-42298-4	Sequence 4, App1
11	343	26.3	58	PCT-US05-34335-37	Sequence 37, App1
12	343	26.3	58	US-11-287-121A-4	Sequence 4, App1
13	342	26.2	61	PCT-US05-42298-16	Sequence 16, App1
14	342	26.2	61	PCT-US05-34335-38	Sequence 38, App1
15	342	26.2	61	US-11-287-121A-16	Sequence 16, App1
16	334	25.6	58	PCT-US05-34335-39	Sequence 39, App1
17	320	24.5	60	PCT-US05-34335-51	Sequence 51, App1
18	312	23.9	56	PCT-US05-42298-11	Sequence 11, App1
19	312	23.9	56	US-11-287-121A-11	Sequence 11, App1
20	305	23.4	68	US-60-763-373-177	Sequence 177, App
21	305	23.4	1487	US-60-772-265-1	Sequence 1, App1
22	265	20.3	513	US-11-268-554-187	Sequence 187, App
23	265	20.3	513	US-60-735-818-3	Sequence 3, App1
24	265	20.3	513	US-60-741-050-21	Sequence 21, App1
25	265	20.3	513	US-60-763-365-24	Sequence 24, App1

## ALIGNMENTS

RESULT 1  
US-11-301-554-332  
Sequence 332, Application US/11301554  
GENERAL INFORMATION:  
APPLICANT: Henderson, Robert A.  
APPLICANT: Wang, Tonglong  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Kalos, Michael D.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Johnson, Jeffrey C.  
APPLICANT: Retter, Marc W.  
APPLICANT: Durham, Margarita  
APPLICANT: Carter, Darrick  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: McNabb, Andria  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C21  
CURRENT APPLICATION NUMBER: US/11/301,554  
PRIOR FILING DATE: 2005-12-13  
PRIOR APPLICATION NUMBER: US 10/283,017  
PRIOR FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: US 10/113,872  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 10/017,754  
PRIOR FILING DATE: 2001-10-29  
PRIOR APPLICATION NUMBER: US 09/902,941  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 09/849,626  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: US 09/736,457  
PRIOR FILING DATE: 2000-12-13  
PRIOR APPLICATION NUMBER: US 09/702,705  
PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: US 09/677,419  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 09/671,325  
PRIOR FILING DATE: 2000-09-26  
PRIOR APPLICATION NUMBER: US 09/658,824  
PRIOR FILING DATE: 2000-09-08  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2157  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 332  
LENGTH: 235  
TYPE: PRT

26	265	20.3	513	8	US-60-763-365-26	Sequence 26, App1
27	265	20.3	513	7	US-60-763-374-86	Sequence 86, App1
28	262	20.1	529	8	US-11-268-554-188	Sequence 188, App1
29	262	20.1	529	8	US-60-735-818-1	Sequence 1, App1
30	262	20.1	529	8	US-60-735-818-2	Sequence 2, App1
31	262	20.1	529	8	US-60-763-365-25	Sequence 25, App1
32	262	20.1	529	8	US-60-763-365-27	Sequence 27, App1
33	262	20.1	529	8	US-60-763-374-87	Sequence 87, App1
34	217.5	16.7	252	7	US-11-268-554-118	Sequence 118, App
35	217.5	16.7	252	7	US-11-268-554-119	Sequence 119, App
36	217.5	16.7	252	7	US-11-342-366-1027	Sequence 1027, App
37	217.5	16.7	252	7	US-11-342-367-1027	Sequence 1027, App
38	193.5	14.8	595	8	US-60-772-265-1087	Sequence 1087, App
39	186	14.2	58	1	PCT-US05-42298-19	Sequence 19, App1
40	186	14.2	58	1	PCT-US05-34335-34	Sequence 34, App1
41	186	14.2	58	7	US-11-287-121A-19	Sequence 19, App1
42	180	13.8	352	6	US-10-567-867-1411	Sequence 1411, App
43	180	13.8	366	6	US-10-498-451-2681	Sequence 2681, App
44	162.5	12.4	2971	8	US-60-741-048-155	Sequence 155, App
45	162.5	12.4	2971	8	US-60-741-048-158	Sequence 158, App

```
; ORGANISM: Homo sapiens
US-11-301-554-332

Query Match
Best Local Similarity 100.0%; Score 1306; DB 7; Length 235;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDAPRLGISILLPLTEALGDAOEPTGNNAICLLPLDYGPCRALLLRYTDTOS 60
DB 1 MDAPRLGISILLPLTEALGDAOEPTGNNAICLLPLDYGPCRALLLRYTDTOS 60
QY 61 CRQFLYGGCGGNANNFYTWACDQACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSM 120
DB 61 CRQFLYGGCGGNANNFYTWACDQACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSM 120
QY 121 TCCEPFGSGCHRRNIENRFPDEATCMGFCAPKKI PSFCYSPKDEGLCSANVTYFNPRY 180
DB 121 TCCEPFGSGCHRRNIENRFPDEATCMGFCAPKKI PSFCYSPKDEGLCSANVTYFNPRY 180
QY 181 RTCDATFTYTGCGGNDNPNVSRDCKRACAKALKKKKMPRLRPSAIRIRKKQP 235
DB 181 RTCDATFTYTGCGGNDNPNVSRDCKRACAKALKKKKMPRLRPSAIRIRKKQP 235

RESULT 2
US-11-107-643-1
; Sequence 1, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 213
; TYPE: PRT
; ORGANISM: homosapiens
US-11-107-643-1

Query Match
Best Local Similarity 91.9%; Score 1200; DB 7; Length 213;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 60
QY 83 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 142
DB 61 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 120
QY 143 ATCMGFCAPKKI PSFCYSPKDEGLCSANVTYFNPRYTCDAFTYTGCGGNDNPNVSR 202
DB 121 ATCMGFCAPKKI PSFCYSPKDEGLCSANVTYFNPRYTCDAFTYTGCGGNDNPNVSR 180
QY 203 DCKRACAKALKKKKMPRLRPSAIRIRKKQP 235
DB 181 DCKRACAKALKKKKMPRLRPSAIRIRKKQP 213

RESULT 3
US-11-107-643-2
; Sequence 2, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
```

```
; CURRENT APPLICATION NUMBER: US/11/107,643
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 73
; TYPE: PRT
; ORGANISM: homosapiens
US-11-107-643-2

Query Match
Best Local Similarity 32.2%; Score 421; DB 7; Length 73;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 60
QY 83 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 142
DB 61 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 120

RESULT 4
US-11-107-643-3
; Sequence 3, Application US/11107643
; GENERAL INFORMATION:
; APPLICANT: Kistel, Walter
; TITLE OF INVENTION: Human Kunitz-type Inhibitor with Enhanced Antifibrinolytic
; FILE REFERENCE: 310.00170101
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: mutated KD-1
US-11-107-643-3

Query Match
Best Local Similarity 32.0%; Score 418; DB 7; Length 73;
Matches 72; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 82
DB 1 DAAOEPTGNNAICLLPLDYGPCRALLLRYTDTOSCRQFLYGGCGGNANNFYTWAC 60
QY 83 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 142
DB 61 DDACWRIEKVPKQRLQVSVDQCEGSTEKYPNLSMTCCEPFGSGCHRRNIENRFPDE 120

RESULT 5
PCT-US05-42298-1
; Sequence 1, Application PCT/US0542298
; GENERAL INFORMATION:
; APPLICANT: Dyax Corporation
; TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES
; FILE REFERENCE: 10280-122W01
; CURRENT APPLICATION NUMBER: PCT/US05/42298
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: US 60/630,226
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
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ORGANISM: Homo sapiens  
PCT-US05-42298-1

29.7%; Score 388; DB 1; Length 304;

```

QY 12 LLELFTEALDAAOE-----PGNNAEICLEPLDGPCCALLRYDYBYT 58
Db 17 LLLNAPAPLNADSEEDBEHHTIYDTPLPLKMHSPCAFDADGCPCAIMKRPFFNIPT 76
QY 59 QSCROPLYGCGEGANNFYTWACDDACWR-----IEKPKYCRLOQSVDDO-- 105
Db 77 RQCEFFITGCGEGONRRESLEECCKMOTRNNARIITKTLQOEKEDPCFLE--EDPGI 133
QY 106 CEGSTBKCFPLMSWTECKFPSSGGCHRRIRIENRPFDEATCMGFC----- 149
Db 134 CRGIIITRYFTNNQTKOCERFKYGGCLGM--NNFTLEECKNICEDGPNGFQVDNYGTQL 191
QY 150 -----APKKI-----PSFCVSPKDEGLCSANVTYYFNPRYRTCDAPTYTGC 192
Db 192 NAYVNSLTPPOSTKYVSLFEFHGPGSWCLTPADRGICRAIENHFFYNSVIGKCRPFYSGCG 251
QY 193 GNDNPFVSRDCKRACAKAL-----KKKKKPKLRFA 224
Db 252 GNENNFTSKQECLEPCKCKKGFPTORISKGLITTKRRKKORVYIA 295

```

RESULT 6  
PCT-US05-34335-54

Query Match	29.7%	Score 388	DB 1	Length 304
Best Local Similarity	30.3%	Pred. No. 2.8e-30		
Matches 86	Conservative 37	Mismatches 85	Indels 76	Gaps 8

```

Oy 12 LILFTEALGPAAC-----PTGNNABICLLPLVYGCRRALLRYDYRYT 58
Db 17 LLINTAPADLNDSEDEDEHTITDTLEPLPKLMHSPCAKADGCPKALIMKRPFFNIPT 76
Oy 59 OGRCPVLVYGGCGGNANFYTWEACDDACWR-----IEKVPKVCLOYSVDQ-- 105
Db 77 ROCBEEITYGGCGGNORFESBLECKKCKCTRDANRIIKTTLQCKPDCLE--EDPGI 133
Oy 106 CEGSTERYEPNLISMTCEKFPSSGCHRNRIENRPDEATCMGFC----- 149
Db 134 CRGYITRYYYNNOQKOCERPKYGGCLGNM--NNFETLEBCKNICEDDPNGFOVDNYGTOL 191
Oy 150 -----APKKI-----PSFCYSPDEGLCSANVRYYPNRPYRTCDATFYTGCG 192
Db 192 NAYVNSLTQSTVPSLFEFHGFSWCLTPADRLGRANENRPYYNSIYGKCRPFKYSGCG 251
Oy 193 GNDNPFVSRDECKRACAKAL-----KKGGMPQLRFA 224

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Db 252 GNENFTSKQECRLACKGFIQIRISKGLIKTKRKRKKQVKA 2955

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RESULT 7
US-11-287-121A-1
; Sequence 1, Application US/11287121A
; GENERAL INFORMATION:
; APPLICANT: Deyv, Laetitia
; APPLICANT: Ley, Arthur C.
; APPLICANT: Ledner, Robert C.
; TITLE OR INVENTION: PLASMIN-INHIBITORY THERAPIES
; FILE REFERENCE: 10280-122001
; CURRENT APPLICATION NUMBER: US/11/287,121A
; CURRENT FILING DATE: 2005-11-22
; PRIOR APPLICATION NUMBER: US 60/630,226
; PRIOR FILING DATE: 2004-11-22
; NUMBER OF SEQ. ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-287-121A-1

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Query Match 29.7%; Score 388; DB 7; length 304;  
Best Local Similarity 30.3%; Pred. No. 2.8e-30;  
Matches 86; Conservative 37; Mismatches 85; Indels 76; Gaps 8

```

Qy 1 LLLFLTEALGSAAG-----PGNNABICLPLDYGPCRALILRYDYRT 58
Db 17 LILNLPALPLANDSEDEBHTITDTPLPLKLMHSCAFPAADGFCALIMKRFNFIPT 76
Qy 59 QSGROPLYGCGEGNANNFYTWACDAMC-----IEKPYKVCLOVSVDQ-- 105
Db 77 ROCERETIYGGCEGNOHREFSELECKCKMCTRDNANRIITKTLQOEKDPDFCELE--EDPGI 133
Qy 106 CESETEKYEPNLSMTCEKFPSCGCHRRIRENRPDEATCMGFC----- 148
Db 134 CRGIITRITRYNNOTKOCERFKYGGGLGNN--INBETLECKNITCEDGPNQVDNVTOL 191
Qy 150 -----APKCI-----PSCYSPKDEGLCSANVTYYNPRYTCDAFTYTCG 192
Db 192 NAVNNSILTFQSTKVPSLFEFHGFPSCWLPADRGICRAENENFYNSVYGKCRPXPYGGCG 251
Qy 193 GNNNVFSREDCKRAAKAL-----KXKKKMPKRF 224
Db 252 GNNNFTSKQECIRACKGFPRIJSKGLITKRRGKKORQYXIA 295

```

```

RESULT 8
US-11-302-208-1
; Sequence 1, Application US/11302208
; GENERAL INFORMATION:
; APPLICANT: Chen, Bao-Lu
; APPLICANT: Huang, Chin-Yi
; TITLE OF INVENTION: Stabilized Compositions Comprising Tissue Factor Pathway Inhibitor
; TITLE OF INVENTION: Protein or Tissue Factor Pathway Inhibitor Variant Proteins
; FILE REFERENCE: 12441.00054
; CURRENT APPLICATION NUMBER: US/11/302,208
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/753,068
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/438,519
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US 60/474,577
; PRIOR FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: US 60/509,260
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/512,090
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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LENGTH: 276  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-302-208-1

Query Match 29.4%; Score 384.5; DB 7; Length 276;  
Best Local Similarity 31.6%; Pred. No. 5.5e-30;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLPLDYGPGRALLIRYYDRYTGSCROFLYGCCEGNANFNFTWACDDACMR-----88  
DB 26 CAPKADGCKAIKMKFFFNITRQCEBFIYGCCEGNORFESLECKMKCTRDANRII 85  
QY 89 ----LEKVPKVLQVSVDDQ--CEGSTEKYEFNLSMTCEKFFSGGCHRNRIENRFPDE 142  
DB 86 KTTLOEKNDPFCFLE---EDPGICRGYITRYFYNNQTKQCEKFKYGGCLGNM--NNFETL 140  
QY 143 ATCMGFC-----APKTI-----PSFCYSPDGLCSA 169  
DB 141 BECKNICEDGPNQFQVDNYGTOLNANVNSLTPQSTKVPSLFEFHGSPWCLTPADRLGCPA 200  
QY 170 NTRYFYENPRYATCDAFYTYGCGGNDNPNVSRDCGRACAKL-----KCKKK 217  
DB 201 NENRFFYNISVIGCKRPFKISGCGENNNFTSKQCLPACCKGFIQRIKGLIKTKRKXK 260  
QY 218 MPELRPA 224  
DB 261 KORVKIA 267

RESULT 9  
US-11-337-518-1  
Sequence 1, Application US/11337518

GENERAL INFORMATION:

APPLICANT: Dorin, Glenn J.  
APPLICANT: Arve, Bo H.  
APPLICANT: Patlison, Gregory J.  
APPLICANT: Halenbeck, Robert F.  
APPLICANT: Johnson, Kirk  
APPLICANT: Chen, Bao-lu  
APPLICANT: Bana, Ralsharan K.  
APPLICANT: Hora, Maninder S.  
APPLICANT: Madani, Haasan  
APPLICANT: Teang, Michael  
APPLICANT: Gustafson, Mark E.  
APPLICANT: Bidd, Gary S.  
APPLICANT: Johnson, Gary V.  
TITLE OF INVENTION: Formulation, Solubilization, Purification, and Refolding of Tissue  
TITLE OF INVENTION: Pathway Inhibitor  
FILE REFERENCE: 012441.00013  
CURRENT APPLICATION NUMBER: US/11/337,518  
CURRENT FILING DATE: 2006-01-24  
PRIOR APPLICATION NUMBER: US/09/996,588  
PRIOR FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: US 08/477,677  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: US 08/473,668  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: PCT/US96/09980  
PRIOR FILING DATE: 1996-06-07  
PRIOR APPLICATION NUMBER: US 09/973,211  
PRIOR FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: US 09/443,099  
PRIOR FILING DATE: 1999-11-18  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 276  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-337-518-1

Query Match 29.4%; Score 384.5; DB 7; Length 276;

Best Local Similarity 31.6%; Pred. No. 5.5e-30;  
Matches 78; Conservative 35; Mismatches 71; Indels 63; Gaps 7;

QY 36 CLPLDYGPGRALLIRYYDRYTGSCROFLYGCCEGNANFNFTWACDDACMR-----88  
DB 26 CAPKADGCKAIKMKFFFNITRQCEBFIYGCCEGNORFESLECKMKCTRDANRII 85  
QY 89 ----LEKVPKVLQVSVDDQ--CEGSTEKYEFNLSMTCEKFFSGGCHRNRIENRFPDE 142  
DB 86 KTTLOEKNDPFCFLE---EDPGICRGYITRYFYNNQTKQCEKFKYGGCLGNM--NNFETL 140  
QY 143 ATCMGFC-----APKTI-----PSFCYSPDGLCSA 169  
DB 141 BECKNICEDGPNQFQVDNYGTOLNANVNSLTPQSTKVPSLFEFHGSPWCLTPADRLGCPA 200  
QY 170 NTRYFYENPRYATCDAFYTYGCGGNDNPNVSRDCGRACAKL-----KCKKK 217  
DB 201 NENRFFYNISVIGCKRPFKISGCGENNNFTSKQCLPACCKGFIQRIKGLIKTKRKXK 260  
QY 218 MPELRPA 224  
DB 261 KORVKIA 267

RESULT 10  
PCT-US05-42298-4  
Sequence 4, Application PC/TUS0542298

GENERAL INFORMATION:

APPLICANT: Dyax Corporation  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122WO1  
CURRENT APPLICATION NUMBER: PCT/US05/42298  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-42298-4

Query Match 26.3%; Score 343; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 NAEICLPLDYGPGRALLIRYYDRYTGSCROFLYGCCEGNANFNFTWACDDACMR 89  
DB 1 NAEICLPLDYGPGRALLIRYYDRYTGSCROFLYGCCEGNANFNFTWACDDACMR 58

RESULT 11  
PCT-US05-34335-37  
Sequence 37, Application PC/TUS0534335

GENERAL INFORMATION:

APPLICANT: Blait, Henry  
APPLICANT: Beck, Thomas  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THROMBOLYTIC AGENTS AND USES THEREOF  
FILE REFERENCE: 10280-131WO1  
CURRENT APPLICATION NUMBER: PCT/US05/34335  
CURRENT FILING DATE: 2005-09-22  
PRIOR APPLICATION NUMBER: US 11/125,639  
PRIOR FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US 10/953,902  
PRIOR FILING DATE: 2004-09-27  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 58

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-34335-37

Query Match 26.3%; Score 343; DB 1; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 NAEICLLPVDGECRALLRLRYYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 89  
DB 1 NAEICLLPVDGECRALLRLRYYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 58

RESULT 12  
US-11-287-121A-4  
Sequence 4, Application US/11287121A  
GENERAL INFORMATION:  
APPLICANT: Dey, Laetitia  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: US/11/287,121A  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 58  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-11-287-121A-4

Query Match 26.3%; Score 343; DB 7; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.2e-26;  
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 NAEICLLPVDGECRALLRLRYYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 89  
DB 1 NAEICLLPVDGECRALLRLRYYYDRYTQSCROFLYGCCEGNANFTYWEACDQACWRI 58

RESULT 13  
PCT-US05-42298-16  
Sequence 16, Application PC/TUS0542298  
GENERAL INFORMATION:  
APPLICANT: Dyax Corporation  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: PCT/US05/42298  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-42298-16

Query Match 26.2%; Score 342; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 92 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 151

DB 1 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 60  
QY 152 K 152  
DB 61 K 61

RESULT 14  
PCT-US05-34335-38  
Sequence 38, Application PC/TUS0534335  
GENERAL INFORMATION:  
APPLICANT: Blair, Henry  
APPLICANT: Beck, Thomas  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: KALLIKREIN INHIBITORS AND ANTI-THROMBOLYTIC AGENTS AND USES THEREOF  
FILE REFERENCE: 10280-131M01  
CURRENT APPLICATION NUMBER: PCT/US05/34335  
CURRENT FILING DATE: 2005-09-22  
PRIOR APPLICATION NUMBER: US 11/125,639  
PRIOR FILING DATE: 2005-05-09  
PRIOR APPLICATION NUMBER: US 10/953,902  
PRIOR FILING DATE: 2004-09-27  
NUMBER OF SEQ ID NOS: 56  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
PCT-US05-34335-38

Query Match 26.2%; Score 342; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 151  
DB 1 VPKVCLQVSDVDDQCGSTGTEKTFPNLSMTCKEFGGCHRRNIENRPFDEATCMGFCAP 60

QY 152 K 152  
DB 61 K 61

RESULT 15  
US-11-287-121A-16  
Sequence 16, Application US/11287121A  
GENERAL INFORMATION:  
APPLICANT: Dey, Laetitia  
APPLICANT: Ley, Arthur C.  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: PLASMIN-INHIBITORY THERAPIES  
FILE REFERENCE: 10280-122001  
CURRENT APPLICATION NUMBER: US/11/287,121A  
CURRENT FILING DATE: 2005-11-22  
PRIOR APPLICATION NUMBER: US 60/630,226  
PRIOR FILING DATE: 2004-11-22  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetically generated peptide  
US-11-287-121A-16

Query Match 26.2%; Score 342; DB 7; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy	92	VPKVCRLQVSVDDQCEGSTEKYPFNLSMTCEKFPFGGCHRNRIENRFPDEATCMGFCAP	151
Db	1	VPKVCRLQVSVDDQCEGSTEKYPFNLSMTCEKFPFGGCHRNRIENRFPDEATCMGFCAP	60
Qy	152	K 152	
Db	61	K 61	

Search completed: March 9, 2006, 20:08:42  
Job time : 40 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 05:24:57 ; Search time 5415 Seconds  
(without alignments)  
10276.960 Million cell updates/sec

Title: US-10-800-057-1

Perfect score: 979  
Sequence: 1 ggaagccttgccgcagcgsggc.....ctgttcttgagactgaattc 979

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_sbs: \*  
11: gb\_ey: \*  
12: gb\_un: \*  
13: gb\_vl: \*  
14: gb\_hlg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	979	100.0	979	E34398
2	979	100.0	979	E34460
3	979	100.0	979	E34460
4	979	100.0	979	E34460
5	979	100.0	979	E34460
6	979	100.0	979	E34460
7	979	100.0	979	E34460
8	979	100.0	979	E34460
9	979	100.0	979	E34460
10	979	100.0	979	E34460
11	979	100.0	979	E34460
12	979	100.0	979	E34460
13	979	100.0	979	E34460
14	979	100.0	979	E34460
15	979	100.0	979	E34460
16	979	100.0	979	E34460
17	979	100.0	979	E34460
18	979	100.0	979	E34460

19	898.2	91.7	1736	8	AK092499	AK092499 Homo sapi
20	863.4	88.2	941	6	AX704793	AX704793 Sequence
21	845.4	86.4	2308	6	AX147515	AX147515 Sequence
22	815.4	83.3	2110	6	AX147516	AX147516 Sequence
23	800.2	81.7	1088	6	AK075425	AK075425 Homo sapi
24	793	75.5	924	8	BC034155	BC034155 Homo sapi
25	682	69.7	728	8	AK024817	AK024817 Homo sapi
26	557.8	57.0	1057	6	AX147525	AX147525 Sequence
27	540.8	55.2	593	6	BD059110	BD059110 Secreted
28	516.4	52.7	1339	4	AY234861	AY234861 Bos tauru
29	447	45.7	528	6	AR272352	AR272352 Sequence
30	447	45.7	528	6	AR275933	AR275933 Sequence
31	447	45.7	528	6	AR406208	AR406208 Sequence
32	447	45.7	528	6	AR440058	AR440058 Sequence
33	447	45.7	528	6	AR472217	AR472217 Sequence
34	447	45.7	528	6	AR542869	AR542869 Sequence
35	447	45.7	528	6	AR638027	AR638027 Sequence
36	447	45.7	528	6	AX062437	AX062437 Sequence
37	447	45.7	528	6	AX673554	AX673554 Sequence
38	424.8	43.4	476	6	CO406709	CO406709 Sequence
39	348	35.5	1521	10	BV179049	BV179049 sgm10366
40	334.4	34.2	464	10	G27880	G27880 human SRS S
41	312	31.9	8173	8	AF217542	AF217542 Homo sapi
42	310.4	31.7	149764	8	AC002076	AC002076 Homo sapi
43	310.4	31.7	194395	14	AC084370	AC084370 Homo sapi
44	294.6	30.1	145206	14	AC096850	AC096850 Pan trogl
45	294.6	30.1	173047	8	AC146007	AC146007 Pan trogl

#### ALIGNMENTS

RESULT 1  
LOCUS E34398 979 bp DNA linear PAT 31-JAN-2002  
DEFINITION Vascular smooth muscle proliferator.  
ACCESSION E34398  
VERSION E34398.1 GI:18624343  
KEYWORDS JP 2000128802-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 979)  
AUTHORS Yui, Y.  
TITL Vascular smooth muscle Proliferator  
JOURNAL Patent: JP 2000128802-A 09-MAY-2000;  
SHIONOGI & CO LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2000128802-A/1  
PD 09-MAY-2000  
PF 19-OCT-1998 JP 1998296760  
PR

YOSHIMI YUI  
PC A61K38/55, A61K31/00, A61K38/00, C07K14/47, C12N15/09,  
PC C12Q1/68,  
PC A61K37/64, A61K37/02, C12N15/00  
CC  
FH Key Location/Qualifiers  
FT CDS (39) . (743) .  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

#### ORIGIN

Query Match 100.0%; Score 979; DB 6; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.6e-216; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GAGACCCCTTGGCCACGCGGCGCCGACCCCTTGACCACTGACCCCGCTCCCGCCCTGG 60  
 Oy 61 GGGCTGCAATTCGTGCTTTCTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
 Db 61 GGGCTGCAATTCGTGCTTTCTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
 Oy 121 CAACAGAAATTAACCGGAGATCTGCTTCCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 Db 121 CAACAGAAATTAACCGGAGATCTGCTTCCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 Oy 181 TACTTCTCCGTTACTACTACGACAGTACAGGACGCTGCCCTGACCTACGAGACCTGCGGGGCC 240  
 Db 181 TACTTCTCCGTTACTACTACGACAGTACAGGACGCTGCCCTGACCTACGAGACCTGCGGGGCC 240  
 Oy 241 GCTGCGAGGCGACCCGCAACATTTCTACCTGGAGGCTTGGACGATGCTGCTGCTGCA 300  
 Db 241 GCTGCGAGGCGACCCGCAACATTTCTACCTGGAGGCTTGGACGATGCTGCTGCTGCA 300  
 Oy 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTACAGGACGCTGCCGCTGTAAGGAGG 360  
 Db 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTACAGGACGCTGCCGCTGTAAGGAGG 360  
 Oy 361 GGTCCACAGAAAGTATTTCTTATCTTAAGTTCATGACATGAGTGAAGAAATTTCTTTCCG 420  
 Db 361 GGTCCACAGAAAGTATTTCTTATCTTAACTTCAATGATGTAAGAAATTTCTTTCCG 420  
 Oy 421 GTGGGTGTCAACCGGACCGGATGAGAGAGGTTCCAGATGAGCTACTGTATGAGGCT 480  
 Db 421 GTGGGTGTCAACCGGACCGGATGAGAGAGGTTCCAGATGAGCTACTGTATGAGGCT 480  
 Oy 481 TCTGCGCACCAAGAAATTCATTTTGTCTGCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Db 481 TCTGCGCACCAAGAAATTCATTTTGTCTGCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Oy 541 CTGCAAGTATCTGCTATTTTATTTTATCCAAAGTACAGAACTGTATGCTTTCACT 600  
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 Oy 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTCCGCTTCCAGTAAATCC 720  
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 Oy 721 GGAATAATTCGGAAGAGATTTTAAATCTTAATGTCATGCTGTTGTCTTTATG 780  
 Db 721 GGAATAATTCGGAAGAGATTTTAAATCTTAATGTCATGCTGTTGTCTTTATG 780  
 Oy 781 GCTTATTTGCTTTATGCTGATCTGAAGATTAATGACAGATGAGAAACAAATCA 840  
 Db 781 GCTTATTTGCTTTATGCTGATCTGAAGATTAATGACAGATGAGAAACAAATCA 840  
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 Db 841 TTGGGATTTATTCACCAAGTTTATTAATCAAGTCACTTTTCAAAAAATTTGGAATTT 900  
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 Db 901 TTTATATTAATCTAGCTGCTATGCAAAATGATGCACTTTTAAATTAATGCTGCAAC 960  
 Oy 961 TGTGTCAGACTGAATTC 979  
 Db 961 TGTGTCAGACTGAATTC 979

RESULT 2  
 E34460 979 bp DNA linear PAT 31-JAN-2002  
 LOCUS E34460  
 DEFINITION Tissue factor pathway inhibitor-2 antibody.  
 ACCESSION E34460

VERSION E34460.1 GI:18624347  
 KEYWORDS JP 2000128803-A/1.  
 SOURCES Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 Yui, Y.  
 Tissue factor pathway inhibitor-2 antibody  
 Patent: JP 2000128803-A 1 09-MAY-2000;  
 SHIONOGI & CO LTD  
 OS Homo sapiens (human)  
 PN JP 2000128803-A/1  
 PD 09-MAY-2000  
 PR 19-OCT-1998 JP 1998296759  
 CC  
 PI YOSHIMI YUI  
 PC A61K39/395, A61K39/395, A61K31/00, A61K31/00, C07K16/36, C12N5/10,  
 PC C12N15/09,  
 PC C12P21/02, G01N33/50, G01N33/53 // (C12P21/02, C12R1.91), C12N5/00,  
 PC C12N15/00  
 CDS  
 FH Key Location/Qualifiers  
 FT CDS (39)..(743).  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
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 ORIGIN  
 Query Match 100.0%; Score 979; DB 6; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-216;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GAGACCCCTTGGCCACGCGGCGCCGACCCCTTGACCACTGACCCCGCTCCCGCCCTGG 60  
 Db 1 GAGACCCCTTGGCCACGCGGCGCCGACCCCTTGACCACTGACCCCGCTCCCGCCCTGG 60  
 Oy 61 GGGCTGCAATTCGTGCTTTCTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
 Db 61 GGGCTGCAATTCGTGCTTTCTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
 Oy 121 CAACAGAAATTAACCGGAGATCTGCTTCCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 Db 121 CAACAGAAATTAACCGGAGATCTGCTTCCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 Oy 181 TACTTCTCCGTTACTACTACGACAGTACAGGACGCTGCCCTGACCTACGAGACCTGCGGGGCC 240  
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 Db 241 GCTGCGAGGCGACCCGCAACATTTCTACCTGGAGGCTTGGACGATGCTGCTGCTGCA 300  
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 Db 301 GGAATGAAAAAGTTCCAAAGTTTCCGCGCTGCAAGTACAGGACGCTGCCGCTGTAAGGAGG 360  
 Oy 361 GGTCCACAGAAAGTATTTCTTATCTTAACTTCAATGATGTAAGAAATTTCTTTCCG 420  
 Db 361 GGTCCACAGAAAGTATTTCTTATCTTAACTTCAATGATGTAAGAAATTTCTTTCCG 420  
 Oy 421 GTGGGTGTCAACCGGACCGGATGAGAGAGGTTCCAGATGAGCTACTGTATGAGGCT 480  
 Db 421 GTGGGTGTCAACCGGACCGGATGAGAGAGGTTCCAGATGAGCTACTGTATGAGGCT 480  
 Oy 481 TCTGCGCACCAAGAAATTCATTTTGTCTGCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Db 481 TCTGCGCACCAAGAAATTCATTTTGTCTGCTCAAGTCCAAAGATGAGGAGCTGTCT 540  
 Oy 541 CTGCAAGTATCTGCTATTTTATTTTATCCAAAGTACAGAACTGTATGCTTTCACT 600

Db 541 CTGCAATGTAAGTCTGTAATTAATTCAGAAATGATGATCTTCACT 600  
 Qy 601 ATACTGCTGAGAGGAAATGACATTAATTTGTAAGAGAGATGTCAAAGTCAT 660  
 Db 601 ATACTGCTGAGAGGAAATGACATTAATTTGTAAGAGAGATGTCAAAGTCAT 660  
 Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTCGCTTCCAGTAGAATCC 720  
 Db 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTCGCTTCCAGTAGAATCC 720  
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 Db 721 GGAATATTCGAGAGAGCAATTTTAAACATTCTTAATATGTCATCTTGTCTTAA 780  
 Qy 781 GCTATTGCTTATGCTTATCTGTAAGAAATATATGACAGATGAGAAACAAATCA 840  
 Db 781 GCTATTGCTTATGCTTATCTGTAAGAAATATATGACAGATGAGAAACAAATCA 840  
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 Db 841 TTGGGATTTATTCACAGCTTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTT 900  
 Qy 901 TTATATATTAAGTCTGCTATTCATATGATGAGTCTACATTTTAAATTAATGTTCAAC 960  
 Db 901 TTATATATTAAGTCTGCTATTCATATGATGAGTCTACATTTTAAATTAATGTTCAAC 960  
 Qy 961 TGTTTGTGAGACTGAATTC 979  
 Db 961 TGTTTGTGAGACTGAATTC 979

## RESULT 3

LOCUS 114875 979 bp DNA linear PAT 02-APR-1996  
 DEFINITION Sequence 1 from patent US 5455338.  
 ACCESSION 114875  
 VERSION 114875.1 GI:1249784  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 979)  
 Srecher C.A., Kistiel, W. and Foster, D.C.  
 TITLE DNA encoding a novel human kunitz-type inhibitors and methods  
 relating thereto  
 JOURNAL Patent US 5455338-A 1 03-OCT-1995;  
 FEATURES Location/Qualifiers  
 source 1..979  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 979; DB 6; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1,66-216; Mismatches 0; Indels 0; Gaps 0;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 GAGAGCTTGGCCAGCGGAGCGGAGCCCTGACCATGACCCGCTGCGCCCTGG 60  
 Qy 61 GAGCTGCTGATTTCTGCTTTTCCGAGAGAGCTGCACTGGGAGATCTGTCAGAGC 120  
 Db 61 GAGCTGCTGATTTCTGCTTTTCCGAGAGAGCTGCACTGGGAGATCTGTCAGAGC 120  
 Qy 121 CAACAGAAATTAACGCGAGATCTGCTGCGCCCTGACCTACGAGACCTGCGCGGCC 180  
 Db 121 CAACAGAAATTAACGCGAGATCTGCTGCGCCCTGACCTACGAGACCTGCGCGGCC 180  
 Qy 181 TACTTCTCGTTACTACTACGACAGGTACAGCAGAGCTGCGCGAGTTCTGTACGAGG 240  
 Db 181 TACTTCTCGTTACTACTACGACAGGTACAGCAGAGCTGCGCGAGTTCTGTACGAGG 240

Qy 241 GCTGAGAGGAGCAAGCAATTTCTACCTGAGAGGCTTGGCAGCATGCTTGTGGA 300  
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 Db 361 GGTGCAAGAAAGTATTTCTTAATCTAAGTTCATGACATGAGAAATTTCTTTCCG 420  
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 Db 541 CTGCAATGATGCTGCTATTAATTCAGATACAGAACTGTGATGCTTCACT 600  
 Qy 601 ATACTGCTGAGAGGAAATGACATTAATTTGTAAGAGAGATGCAAACTGTGAT 660  
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 Qy 781 GCTATTGCTTATGCTTATCTGTAAGAAATATATGACAGATGAGAAACAAATCA 840  
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 Qy 841 TTGGGATTTATTCACAGCTTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTT 900  
 Db 841 TTGGGATTTATTCACAGCTTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTT 900  
 Qy 901 TTATATATTAAGTCTGCTATTCATATGATGAGTCTACATTTTAAATTAATGTTCAAC 960  
 Db 901 TTATATATTAAGTCTGCTATTCATATGATGAGTCTACATTTTAAATTAATGTTCAAC 960  
 Qy 961 TGTTTGTGAGACTGAATTC 979  
 Db 961 TGTTTGTGAGACTGAATTC 979

## RESULT 4

LOCUS 192685 979 bp DNA linear PAT 01-DEC-1998  
 DEFINITION Sequence 1 from patent US 5728674.  
 ACCESSION 192685  
 VERSION 192685.1 GI:3937155  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 979)  
 Srecher C.A., Kistiel, W. and Foster, D.C.  
 TITLE Inhibition of blood coagulation by human-kunitz-type inhibitors  
 JOURNAL Patent US 5728674-A 1 17-MAR-1998;  
 FEATURES Location/Qualifiers  
 source 1..979  
 /organism="unknown"  
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## ORIGIN

Query Match 100.0%; Score 979; DB 6; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.6e-216;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAGAGCCCTGGCCAGAGGCGCGCCGACCCCTGACAGTGAACCCCGTGGCCCCCTGG 60  
1 GAGAGCCCTGGCCAGAGGCGCGCCGACCCCTGACAGTGAACCCCGTGGCCCCCTGG 60  
61 GGCTGTCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
61 GGCTGTCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120  
121 CAACGAGAAATACCGCGAGATCTGTCTGCCCCCTGAGCTACGAGACCTGGCCGCC 180  
121 CAACGAGAAATACCGCGAGATCTGTCTGCCCCCTGAGCTACGAGACCTGGCCGCC 180  
181 TACTTCTCGTTACTACTACGACAGGTACAGGACGCGCGAGTTCCTGTACGCGGG 240  
181 TACTTCTCGTTACTACTACGACAGGTACAGGACGCGCGAGTTCCTGTACGCGGG 240  
241 GCTGCGAGGCGACGCAACATTTCTACCTGGAGGCTTTCGACGATGCTTGGTGA 300  
241 GCTGCGAGGCGACGCAACATTTCTACCTGGAGGCTTTCGACGATGCTTGGTGA 300  
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301 GGAATGAAAAAGTTCCAAAGTTTCCGCTGCAAGTGAAGTGAAGCAACAGTGTAGG 360  
361 GATCAGAGAAAGTATCTTTATCTAAGTTCAGTACATGTGAATAATCTTTTCCG 420  
361 GATCAGAGAAAGTATCTTTATCTAAGTTCAGTACATGTGAATAATCTTTTCCG 420  
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481 TCTGGGCAACCAAGAAATTCATCTTTGTCTACAGTCCAAAGATAGAGGAGCTGTCT 540  
481 TCTGGGCAACCAAGAAATTCATCTTTGTCTACAGTCCAAAGATAGAGGAGCTGTCT 540  
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DEFINITION Sequence 1378 from patent US 6500938.  
ACCESSION AR270815  
VERSION AR270815.1 GI:29702049  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
REFERENCE  
1 (bases 1 to 979)  
AUTHORS Au-Young, J. and Seilhamer, J.J.  
TITLE Composition for the detection of signaling pathway gene expression  
JOURNAL Patent: US 6500938-A 1378 31-DEC-2002;  
Incyte Genomics, Inc.; Palo Alto, CA;  
MOX;

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 DEFINITION Sequence 1 from patent US 6656746.  
 ACCESSION AR437163  
 VERSION AR437163.1 GI:40200260  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 979)  
 Sprechter, C.A., Kisel, W., and Foster, D.C.  
 Antibodies to human kunitz-type inhibitor  
 Patent: US 6656746-A 1 02-DEC-2003;  
 JOURNAL ZymoGenetics, Inc. and University of New Mexico, Seattle, WA  
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## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1,6e-216;  
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## RESULT 7

HUMHTRP 979 bp mRNA linear PRI 27-JUL-1994  
 LOCUS HUMHTRP  
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 ACCESSION L27624  
 VERSION L27624.1 GI:441149  
 KEYWORDS tissue factor pathway inhibitor-2.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 979)  
 Sprechter, C.A., Kisel, W., Mathewes, S., and Foster, D.C.  
 Molecular cloning, expression, and partial characterization of a  
 second human tissue-factor-pathway inhibitor  
 Proc. Natl. Acad. Sci. U.S.A. 91 (8), 3353-3357 (1994)  
 JOURNAL PUBMED 8159751  
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Query Match 100.0%; Score 979; DB 8; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-216;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 VERSION BC005330.1 GI:13529109  
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 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
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 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
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 Scheetz, T.E., Brownstein, M.J., Ugin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.B.,  
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 2 (bases 1 to 1203)

CONSRM  
 TITLE  
 JOURNAL  
 PUBMED  
 REFERENCE  
 AUTHORS  
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 JOURNAL  
 REMARK  
 COMMENT  
 NIH MGC Project  
 Direct Submission  
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 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [gcgaps-remail.nih.gov](mailto:gcgaps-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.  
 M.

FEATURES  
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Query Match 100.0%; Score 979; DB 8; Length 1203;

Best Local Similarity 100.0%; Pred. No. 1.6e-216; Indels 0; Gaps 0;

Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 9

LOCUS CQ412591 2407 bp DNA linear PAT 23-JAN-2004

DEFINITION Sequence 19662 from Patent WO0170979.

ACCESSION CQ412591

VERSION CQ412591.1 GI:41320372

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Lee, J. and Little, J. Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer

JOURNAL Patent: WO 0170979-A 19662/27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)

FEATURES Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

Location/Qualifiers

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Location/Qualifiers

Location/Qualifiers

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QY 361 GGTCACAGAAAAGTATTTCTTAATCTPAAGTTCATGACATGTAAGAAAATTTCTTTCCG 420  
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QY 721 GGAATTAATCGAAGAGCAATTTTAACATTTCTTAATTAATGTCACTGTGTGTCTTTATG 780  
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QY 781 GCTTAATTTGCTTTATGTGTGTATCTGAAGATTAATATGACAGATGAGGAAACAATCA 840  
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RESULT 10  
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LOCUS CQ717511  
DEFINITION Sequence 3445 from Patent WO02068579.  
ACCESSION CQ717511  
VERSION CQ717511.1 GI:42278368  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

ORIGIN  
/db\_xref="taxon:9606"  
Query Match 99.8%; Score 977.4; DB 6; Length 1142;  
Best Local Similarity 99.9%; Pred. No. 3,78-216;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 439 GTGGGTGTCAACCGGAGACCGGATTTGAAGACAGTTTCAAGATGAGCTTGTATGAGGCT 498  
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QY 961 TGTGTGTGAGACTGAATTC 979

Db 979 TGTTCGAGACTGAATTC 997

RESULT 11

AKI29833

LOCUS

DEFINITION Homo sapiens cDNA FLJ26323 f1e, clone HRT00813, highly similar to Tissue factor pathway inhibitor 2 precursor (TFPI-2).

ACCESSION AKI29833

VERSION AKI29833.1 GI:34526454

KEYWORDS oligo capping, f1e (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Suzuki, Y., Hara, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isegai, T. and Sugano, S. NEBO human cDNA sequencing project

JOURNAL Unpublished

TITLE 2 (bases 1 to 2206)

AUTHORS Sugano, S. and Suzuki, Y.

REFERENCE Direct Submission

AUTHORS Submitted (31-JUL-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: f1cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

JOURNAL NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; 3'-end one pass sequencing; RAB; clone selection for full insert sequencing; RAB and Helix Research Institute.

FEATURES

LOCATION/Qualifiers

Source

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/organism="Homo sapiens"

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/note="Cloning vector: pME18SFL3"

ORIGIN

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Best Local Similarity 99.94; Pred. No. 3.8e-216;

Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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2 GGG 97

38 GGAAGCCCTGGCCAGCGGGCCGCGAGCCCTGCAACATGAGCCCGCTGCCCGCTGG 97

61 GGGTGTGAGTTCGCTGCTTTTCTGAGCGAGGCTGCACTGGGCGATGCTGTCAGAGC 120

98 GGGTGTGAGTTCGCTGCTTTTCTGAGCGAGGCTGCACTGGGCGATGCTGTCAGAGC 157

121 CAAAGAGAAATAAGCGGAGATGCTGCTCCCTGAGTACATGAGACCCCTGCCGGGCC 180

158 CAAAGAGAAATAAGCGGAGATGCTGCTCCCTGAGTACATGAGACCCCTGCCGGGCC 217

181 TACTTCTCCGTACTACTACAGAGATGACAGAGAGCTGCCAGTCTCTGTACGGGG 240

218 TACTTCTCCGTACTACTACAGAGATGACAGAGAGCTGCCAGTCTCTGTACGGGG 277

241 GCTGCGAGGGGCAAGCGCAATTTCTACACTGGAGGCTTGGAGAGTCTTGTGGA 300

278 GCTGCGAGGGGCAAGCGCAATTTCTACACTGGAGGCTTGGAGAGTCTTGTGGA 337

Qy 301 GGAATAGAAAAGTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACAGTGTGAG 360

Db 338 GGAATAGAAAAGTCCCAAGTTTCCGCTGCAAGTGAAGTGAACAACAGTGTGAG 397

Qy 361 GGTCCACAGAAAGATATTTCTTAACTAAAGTTCATGACATGTGAATAATCTTTCCG 420

Db 398 GGTCCACAGAAAGATATTTCTTAACTAAAGTTCATGACATGTGAATAATCTTTCCG 457

Qy 421 GTGGGTTCACCCGGAACCGAGATGAGAACAGGTTTCCAGATGAAGTACTTGTATGGGCT 480

Db 458 GTGGGTTCACCCGGAACCGAGATGAGAACAGGTTTCCAGATGAAGTACTTGTATGGGCT 517

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Db 878 TTGGTGAATTAATCAACAGTATTTTAAATTAATCAAGTCACTTTTCAAAAATTTGATTT 937

Qy 901 TTATATATATATAGTCTGCTATTTCAAAATGAGTCTACATTTTAAATTAATGTTCAAC 960

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Qy 961 TGTTCGAGACTGAATTC 979

Db 998 TGTTCGAGACTGAATTC 1016

RESULT 12

AY691946

LOCUS

DEFINITION Homo sapiens tissue factor pathway inhibitor 2 (TFPI2) mRNA, complete cds.

ACCESSION AY691946

VERSION AY691946.1 GI:51475143

KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 1055)

Xu, Y., Li, T. and Du, G.

JOURNAL Direct Submission

TITLE Submitted (21-JUL-2004) Department of Molecular Biology, Medical Research Center, Shenzhen People's Hospital, Medical School of Jnan University, Dongmen North Road 1017, Shenzhen, Guangdong 518020, P.R. China

FEATURES

LOCATION/Qualifiers

Source

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## ORIGIN

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Db	134	CA	AC	GAG	AA	TAA	CG	CG	GA	AT	CT	GT	CT	CG	CC	CT	G	A	CTG	A	CGA	CC	CT	CG	193
Qy	181	TAC	TTCT	CC	GTTA	CTA	CTA	CA	CA	AG	TAA	CA	CG	CA	GA	GCT	CG	CC	CA	GTT	CT	GTA	CG	240	
Db	194	TAC	TTCT	CC	GTTA	CTA	CTA	CA	CA	AG	TAA	CA	CG	CA	GA	GCT	CG	CC	CA	GTT	CT	GTA	CG	253	
Qy	241	GCT	CGA	AGG	CA	CGC	CA	CA	AT	TTCT	CA	CT	TGG	A	AGC	CTT	G	CA	CGAT	GCT	GT	CGA	300		
Db	254	GCT	CGA	AGG	CA	CGC	CA	CA	AT	TTCT	CA	CT	TGG	A	AGC	CTT	G	CA	CGAT	GCT	GT	CGA	313		
Qy	301	GG	AT	G	A	A	A	A	A	A	A	G	T	T	C	C	C	A	A	G	T	T	C	360	
Db	314	GG	AT	G	A	A	A	A	A	A	A	G	T	T	C	C	C	A	A	G	T	T	C	373	
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Db	374	GGT	CCA	CA	G	A	A	A	A	G	T	T	C	T	T	A	T	C	T	A	G	T	T	433	
Qy	421	GT	G	GT	G	T	C	A	C	C	G	A	C	C	G	A	T	T	G	A	A	C	A	480	
Db	434	GT	G	GT	G	T	C	A	C	C	G	A	C	C	G	A	T	T	G	A	A	C	A	493	
Qy	481	TCT	G	G	C	A	C	C	A	A	A	A	T	T	C	A	T	C	A	T	T	T	G	540	
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Qy	541	CTG	CA	A	T	G	A	C	T	CG	CT	A	T	T	A	T	T	A	T	T	C	A	G	600	
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CQ981542				

DEFINITION  
Sequence 397 from Patent EP1398424.  
ACCESSION  
CQ981542  
VERSION  
CQ981542.1 GI:58190832

**KEYWORDS** 'Homo sapiens (human)

ORGANISM  
Homo sapiens  
Bakaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

**AUTHORS** ROSENTHAL, A., HERMANN, K., HEDDEN, E., FILATSKY, C., BRINEMANODOT, I.,  
SCAUB, B., ROEPCKE, S., MENNERICH, D., KINDEMANN, H. and LI, X.  
**TITLE** Human nucleic acid sequences ~~from~~ lung tumours  
**JOURNAL** Patent: EP 1498424-A 397-19-JAN-2005.

FEATURES  
location/Qualifiers  
Hinzmann, Bernd (DB); Germann, Klaus (DB); Heiden, Ismeralda (DB);  
Rosenthal, Andre (DB)

**Source**

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Best Local Similarity	99.7%	Pred. No. 66-215		
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 Db 19 GGAGCGCTTGGCCAGCGGGCCGGCCGACCCCCCTTGACCAATGAGCCCCGCTCGCCCCCTTGG 78  
 Oy 61 GGTGTGATTTCTGCTCTTTTCTGACGAGGCTGCATGGGCGATGCTGCTCAGGAGC 120

Db 79 GGCTGCAATTCTGCTGCTTTTCTGAAGAGCTGCACTGGGCGATGCTGCTCAGAGAC 138

0y 121 CAACAGGAATATACGCGAGATGTGTCTCTGCGCCCTAGACTACGACCCTGCGGGGCC 180

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181 TACTTCTCCGTTACTACTACGACAGGTACACGCAAGTGGCCGCAAGTTCTGTACGGGG 240

Db	199	TACTTCTCCGTTACTACTACGACAGGTACACGACAGAGCTGCCGCGAGTCTCTGTACGGGG	258
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Db 259 GCTGCGAGGGCAACGCCAACAATTTCTACACCTGGAGGCTTGCGACGATGCTTGCTGA 318

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 Db 319 GGATGAGAAAAGTTCCCAAGTTGCGCGCTGCAAGTAGTGTGGACCAACAGGTGAGG 378

361 GGTCCACAGAAAGTATTCTTTAATCTAAGTTCATGCATGTGAAAAATCTTTCCG 420

Db 379 GGTCCACAGAAAGTATTCTTAACTAAGTCCATGCATGTGAAAAATTCTTTCCG 438

QY 421 GTGGGTGTCACCGGAAACCGGATTGAGACAGTTTCCAGATGAAGCTACTTGTATGGGCT 480  
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QY 481 TCTGGGACCAAGAAAGAAATTCATCTTGTGTGCTACAGTCCAAAGATAGAGGAGCTGTGCT 540  
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QY 961 TGTTTGTGAGACTGAT 977  
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RESULT 14  
CS091788 1142 bp DNA linear PAT 03-JUN-2005  
LOCUS CS091788  
DEFINITION Sequence 23 from Patent EP1533619.  
ACCESSION CS091788  
VERSION CS091788.1 GI:66949353  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 Kochan,J.P. and Rosinski,J.A.  
AUTHORS Specific markers for metabolic syndrome  
TITLE Patent: EP 1533619-A 23 25-MAY-2005;  
JOURNAL F. Hoffmann-La Roche AG (CH)  
FEATURES Location/Qualifiers  
SOURCE 1..1142  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

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Best Local Similarity 99.7%; Pred.No.66-215; Indels 3; Gaps 0;

Matches 974; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

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DB 199 TACTTCTCCGTTACTACTAGACAGGTACAGCAGAGCTGCCGCGAGTTCTCTGACGGGG 258  
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DB 379 GGTCCACAGAAAGATTTCTTAAATCTTAAGTTCATGACATGTGAAAAATTTCTTTCG 438  
QY 421 GTGGGTGTCACCGGAAACCGGATTGAGACAGTTTCCAGATGAAGCTACTTGTATGGGCT 480  
DB 439 GTGGGTGTCACCGGAAACCGGATTGAGACAGTTTCCAGATGAAGCTACTTGTATGGGCT 498  
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DB 559 CTGCGAATGTGACTGCTATTATTATTAAATCCAAAGATACAGAACTGTGATGCTTCACTT 618  
QY 601 ATACTGCTGTGAGAGGAAATGACATTAATCTTGTGAGAGGAGATTCGAAACCTGAT 660  
DB 619 ATACTGCTGTGAGAGGAAATGACATTAATCTTGTGAGAGGAGATTCGAAACCTGAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTCGTTTCCAGTAGAATCC 720  
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QY 721 GGAATAATTCGAAAGAGAAATTTAAACATTTCTTAATATATGTCATCTGTGTCTTATAG 780  
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QY 841 TTGGGATTTATTTACCAAGTTTATTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 900  
DB 859 TTGGGATTTATTTACCAAGTTTATTTATTAATCAAGTCACTTTTCAAAAATTTGATTTT 918  
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QY 961 TGTTTGTGAGACTGAT 977  
DB 979 TGTTTGTGAGACTGAT 995

RESULT 15

HMP5 HUMPS 1142 bp mRNA linear PRI 11-JUN-1999  
LOCUS Homo sapiens mRNA for placental protein 5 (Pps), complete cds.  
DEFINITION D29992  
ACCESSION D29992.1 GI:484050  
VERSION Pps; placental protein 5; serine proteinase inhibitor.  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Miyagi,Y., Kohikawa,N., Yasumitsu,H., Miyagi,E., Hirahara,F.,  
Aoki,I., Miyagi,K., Umeda,M. and Miyazaki,K.  
TITLE cDNA cloning and mRNA expression of a serine proteinase inhibitor  
secreted by cancer cells: identification as placental protein 5 and  
tissue factor pathway inhibitor-2  
JOURNAL J. Biochem. 116 (5), 939-942 (1994)  
PUBMED 7895752  
REFERENCE 2 (bases 1 to 1142)  
AUTHORS Miyagi,Y.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-1994) Yohel Miyagi, Yokohama City University  
School of Medicine, Dept. of Pathology, Fukuura 3-9, Kanazawa-ku,  
Yokohama, Kanagawa 226, Japan (Tel:045-787-2587, Fax:045-786-0191)  
Location/Qualifiers  
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Best Local Similarity 99.7%; Pred. No. 6e-215;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGACGCCCTTGGCCAGCGGCGCCGCCGACCCCTGACCAATGAGCCCGCTGCGCCCTTGG 60  
DB 19 GGAAGCCTTGGCCAGCGGCGCGCCGCCGACCCCTGACCAATGAGCCCGCTGCGCCCTTGG 78  
QY 61 GGCTGTGCAATTCGTGCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGC 120  
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QY 121 CAACGAGAAATPACGCGAGATCTGTCTCCCTGACCTAGACCTAGAGCACTGCGCGGCGCC 180  
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DB 259 GCTGCGAGGCGAACCGCAATTCTTCACTCGGAGGCTTGCAGAGATGCTGCTGGA 318  
QY 301 GATGAGAAAGTTCCCAAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGATGAGG 360  
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DB 319 GGATAGAAAAGTTCCAAAGTTGGCCGCTGCAAGTGAAGTGAAGCAACGATGAGG 378  
QY 361 GGTCCACAGAAAAGTATTTCTTAAATCTAAGTTCCATGACATGTGAATAATCTTTCCG 420  
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QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATGACACATGAGAGAAACAAATCA 840  
DB 799 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATGACACATGAGAGAAACAAATCA 858  
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DB 919 TTATATATTAATTAAGTCTGCTATTCATAATGTAGTCTACATTTTAAATTTATGTTCAAC 978  
QY 961 TGTTTGAGACTGAAT 977  
DB 979 TGTTTGAGACTGAAT 995  
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Search completed: March 11, 2006, 07:00:31  
Job time : 5420 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 05:23:21 ; Search time 632 Seconds  
(without alignments)  
10323.946 Million cell updates/sec

Title: US-10-800-057-1

Perfect score: 979

Sequence: 1 ggaagccttcgcacagcg99c.....ctgtcttgagactgaattc 979

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:\*

- 1: geneeqn1980a:\*
- 2: geneeqn1990a:\*
- 3: geneeqn2000a:\*
- 4: geneeqn2001a:\*
- 5: geneeqn2001b:\*
- 6: geneeqn2002a:\*
- 7: geneeqn2002b:\*
- 8: geneeqn2003a:\*
- 9: geneeqn2003b:\*
- 10: geneeqn2003c:\*
- 11: geneeqn2003d:\*
- 12: geneeqn2004a:\*
- 13: geneeqn2004b:\*
- 14: geneeqn2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	979	100.0	979	2	AAQ90469 Human Kun
2	979	100.0	979	10	ACQ56780 Human big
3	979	100.0	979	12	AD156576 Human pol
4	979	100.0	1172	6	ABV94764 Human pan
5	979	100.0	2407	5	ADL45772 Human ova
6	979	100.0	2540	8	ABX63609 Human cdn
7	979	100.0	2540	10	AD156337 Human cdn
8	977.4	99.8	1141	13	AD19178 Human tis
9	977.2	99.3	1142	6	ABX76528 cDNA enco
10	977.2	99.3	1142	8	ABX76528 cDNA enco
11	977.2	99.3	1142	10	ABX08764 Angiogene
12	977.2	99.3	1142	11	ADN38705 Cancer/an
13	977.2	99.3	1142	12	AD183254 Human PRO
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15	977.2	99.3	1142	14	ADZ87319 Human tis
16	961.6	98.2	1075	11	AEA79099 Human apo
17	863.4	86.2	941	8	ABZ76258 Human GEN
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20	732.6	74.8	1162	13	ACN41870 Human dia
21	708	72.3	708	14	ADV42606 Human psy
22	648.4	66.2	651	8	ABZ20345 Group III
23	618	63.1	619	8	ABZ20218 Group III
24	557.8	57.0	1057	5	AAQ6079 Angiotens
25	549.4	56.1	551	8	ABZ20262 Group III
26	540.8	55.2	593	2	AAV86987 EST clone
27	512	52.3	535	8	ABZ20271 Group III
28	509	52.0	509	8	ABZ20248 Group III
29	506.4	51.7	519	8	ABZ20259 Group III
30	502	51.3	502	8	ABZ20251 Group III
31	483	49.3	484	8	ABZ20305 Group III
32	458.6	46.8	495	9	ACH36910 Human end
33	452.8	46.3	489	9	ACH32778 Human end
34	447	45.7	528	5	AAQ68146 Human lun
35	447	45.7	528	6	ABK38057 cDNA enco
36	447	45.7	528	8	ACH10386 Human lun
37	447	45.7	528	8	ABX99337 Lung can
38	447	45.7	528	10	ADH45583 Human lun
39	447	45.7	528	12	ADZ72120 Human lun
40	447	45.7	528	13	AD19502 Human lun
41	439.4	44.9	464	8	ABZ20267 Group III
42	434.8	44.4	502	9	ACH35990 Human end
43	424.8	43.4	476	5	AD139890 Human ova
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## ALIGNMENTS

RESULT 1	AAQ90469	standard; DNA, 979 BP.
ID	AAQ90469	standard; DNA, 979 BP.
AC	AAQ90469;	
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DE	Human Kunitz-type protease-inhibitor TPPI-2 DNL.	
KW	Kunitz-type inhibitor; protease-inhibitor; enzyme-inhibitor;	
OS	anticoagulant; deep vein thrombosis; TPPI-2; de.	
XX	Homo sapiens.	
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XX	W09512674-A1.	
XX	11-MAY-1995.	
XX	02-NOV-1994;	94MO-US012609.
XX	05-NOV-1993;	93US-00147710.
XX	(ZYMO ) ZYMOGENETICS INC.	
XX	(UYNE-) UNIV NEW MEXICO STATE.	
XX	Sprecher CA, Kistiel W, Foster DC;	
XX	WPI, 1995-193821/25.	
XX	P-PSDB; AAR74977.	
XX	Human Kunitz-type protease inhibitors - used as anticoagulants and in the	
XX	treatment of deep vein thrombosis.	
XX	Claim 4; Page 48; 65pp; English.	
XX	This DNA sequence allows for the production of human recombinant Kunitz-	
XX	type protease-inhibitor in large quantities that may be readily purified	



using known methods. The protein encoded by this sequence shares sequence homology and overall domain organization with tissue factor pathway-inhibitor (TFPI), and therefore has been designated TFPI-2

Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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ID ACAS6780 standard; cDNA; 979 BP.

ACAS6780;

06-JUN-2003 (first entry)

Human signalling pathway polynucleotide probe SEQ ID NO 1378.

Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma; leukemia;

immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.

Homo sapiens.

US6500938-B1.

31-DEC-2002.

30-JAN-1998; 98US-00016434.

30-JAN-1998; 98US-00016434.

(INTV-) INCTYE GENOMICS INC.

Au-Young J, Seilhamer JJ;

WPI, 2003-352189/33.

Combination of polynucleotide probes, useful as array elements in a microarray for monitoring the expression of a number of target polynucleotides.

Claim 1; SEQ ID NO 1378; 65pp; English.

The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signalling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=06500938B1

Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 979; DB 10; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGACGCGCTGGCCGAGGCGCGCCGACCCCGGACGATGAGACCCCGCTGCGCCCTGG 60

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Db 1 GAGAGCCTTGGCCAGAGCGGCGCGGACCCCTGACCATGAGACCCGCGCTGCGCCCTG 60  
Qy 61 GGGTGTGCAATCTGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTGAGAGC 120  
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Db 541 CTGCGCAATGTGACTGCTATTAATTTAATCCAGATGACAACTGTGATGCTTCACT 600  
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DT 22-APR-2004 (first entry)  
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DE Human polynucleotide probe #1378.  
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KW Human; probe; se; receptor-like polypeptide; transducing polypeptide;  
KW effector-like polypeptide; cancer; immunopathology; neuropathology;  
KW drug development; toxicology; carcinogenicity;  
KW signalling pathway polypeptide; adrenal gland; bladder; bone;  
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
XX  
OS Homo sapiens.  
XX  
PN US2004010136-A1.  
XX  
PD 15-JAN-2004.  
XX  
PF 26-NOV-2002; 2002US-00305720.  
XX  
PR 30-JAN-1998; 98US-00016434.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Au-Young J, Sellhammer JJ;  
XX  
DR WPI: 2004-090520/09.  
XX  
PT New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.  
XX  
PS Claim 6; SEQ ID NO 1378; 73pp; English.  
XX  
CC The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development.  
CC Microarrays can also be used for monitoring the progression of diseases.  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 979 BP; 258 A; 217 C; 231 G; 273 T; 0 U; 0 Other;

Query Match 100.0%; Score 979; DB 12; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAGCCTTGGCCAGAGCGGCGCGGACCCCTGACCATGAGACCCGCGCTGCGCCCTG 60  
Db 1 GAGAGCCTTGGCCAGAGCGGCGCGGACCCCTGACCATGAGACCCGCGCTGCGCCCTG 60  
Qy 61 GGGTGTGCAATCTGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTGAGAGC 120  
Db 61 GGGTGTGCAATCTGTGCTTTTCTGAGAGGAGGCTGCACTGGGCGATGCTGTGAGAGC 120

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QY 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGGCC 180
DB 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGGCC 180
QY 181 TACTTCTCGTTACTACTACAGAGTACAGGAGTCTGCGGCACTTCTGTACGGG 240
DB 181 TACTTCTCGTTACTACTACAGAGTACAGGAGTCTGCGGCACTTCTGTACGGG 240
QY 241 GCTGAGAGGAGCAAGCAATTTCTACACCTGGAGGCTTGGAGCATGTCTGCTGA 300
DB 241 GCTGAGAGGAGCAAGCAATTTCTACACCTGGAGGCTTGGAGCATGTCTGCTGA 300
QY 301 GGATGAGAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 360
DB 301 GGATGAGAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 360
QY 361 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAATTTCTTTCCG 420
DB 361 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAATTTCTTTCCG 420
QY 421 GTGGGTGTCAACCGGATTTGAGAACGGTTCCAGTGAAGCTACTGTATGGGCT 480
DB 421 GTGGGTGTCAACCGGATTTGAGAACGGTTCCAGTGAAGCTACTGTATGGGCT 480
QY 481 TCTGCGACCAAGAAATTTCCATCATTTTGTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540
DB 481 TCTGCGACCAAGAAATTTCCATCATTTTGTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540
QY 541 CTGCGCAATGTGACTGCTATTTATTTTAACTCAAGATACAGAACTGTGATGCTTTCAGCT 600
DB 541 CTGCGCAATGTGACTGCTATTTATTTTAACTCAAGATACAGAACTGTGATGCTTTCAGCT 600
QY 601 ATACTGCTGTGTGAGGAGTACCAATTAACCTTTAGCAGGAGGATTGCAACGTCAT 660
DB 601 ATACTGCTGTGTGAGGAGTACCAATTAACCTTTAGCAGGAGGATTGCAACGTCAT 660
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGGCTTGTGCTGCAAGTACATCC 720
DB 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGGCTTGTGCTGCAAGTACATCC 720
QY 721 GGAATTTGCGAAGAGCAATTTTAACTTTAATATGTATCTTGTGTCTTTATG 780
DB 721 GGAATTTGCGAAGAGCAATTTTAACTTTAATATGTATCTTGTGTCTTTATG 780
QY 781 GCTTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 840
DB 781 GCTTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 840
QY 841 TTGGTGAATTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAATTTGATTT 900
DB 841 TTGGTGAATTTATTCACAGTTTATTAATATACAGTCACTTTTCAAAATTTGATTT 900
QY 901 TTTATATTAATTAAGTGTATTAATTAATGAGTCTACATTTTAAATTAATGTTTCAAC 960
DB 901 TTTATATTAATTAAGTGTATTAATTAATGAGTCTACATTTTAAATTAATGTTTCAAC 960
QY 961 TGTGTGTGAGACTGAATTC 979
DB 961 TGTGTGTGAGACTGAATTC 979

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RESULT 4  
ABV94764  
ID ABV94764 standard; cDNA; 1172 BP.

AC ABV94764;  
DT 14-JAN-2003 (first entry)

DE Human pancreatic cancer expressed cDNA SEQ ID NO 145.

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;

```

KW cytosolic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
XX
DR P-PSDB; ABP68618.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 1; SEQ ID NO 145; 300pp + Sequence listing; English.
XX
CC The invention relates to an isolated polynucleotide (1) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV9145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published\_pat\_sequences
XX
SQ Sequence 1172 BP; 329 A; 258 C; 263 G; 322 T; 0 U; 0 Other;

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Query Match 100.0%; Score 979; DB 6; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 1.4e-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GAGAGCTTGGCCAGCGGGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTTGG 60
DB 38 GAGAGCTTGGCCAGCGGGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTTGG 97
QY 61 GGCTGTGATTTCTGTGCTTTTCTTGACGAGGCTGCACTGGGCGATGCTGCTACAGAGC 120
DB 98 GGCTGTGATTTCTGTGCTTTTCTTGACGAGGCTGCACTGGGCGATGCTGCTACAGAGC 157
QY 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCGGCTTGAATGAGAACCTTCCGGGGCC 180
DB 158 CAACAGAAATTAACCGGAGATCTGTCTCTGCGGCTTGAATGAGAACCTTCCGGGGCC 217
QY 181 TACTTCTCGTTACTACTACAGAGTACAGGAGTCTGCGGCACTTCTGTACGGG 240
DB 218 TACTTCTCGTTACTACTACAGAGTACAGGAGTCTGCGGCACTTCTGTACGGG 277

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Qy 241 GCTCGAGGAGGAGCAACCAATTTCTACACCTGGAGGCTTGGACGATGCTTGTCTGA 300
Db 278 GCTCGAGGAGGAGCAACCAATTTCTACACCTGGAGGCTTGGACGATGCTTGTCTGA 337
Qy 301 GGATGAGAAAAGTTCCCAAGTTGGCCGGCTGCAAGTAGTGTGACGACCAAGTGTAGG 360
Db 338 GGATGAGAAAAGTTCCCAAGTTGGCCGGCTGCAAGTAGTGTGACGACCAAGTGTAGG 397
Qy 361 GGTCCACGAAAAGTATTTCTTAACTTAAGTCCATGACATGCAAAAATTTCTTTTCCG 420
Db 398 GGTCCACGAAAAGTATTTCTTAACTTAAGTCCATGACATGCAAAAATTTCTTTTCCG 457
Qy 421 GTGGGTGTCACCGGAAACCGGATTGAGACAGGTTCCAGATGAGCTACTGTATGAGGCT 480
Db 458 GTGGGTGTCACCGGAAACCGGATTGAGACAGGTTCCAGATGAGCTACTGTATGAGGCT 517
Qy 481 TCTGGGACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540
Db 518 TCTGGGACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 577
Qy 541 CTGCGCAATGTGACTGCTATTTATTTTATTCAGATGACAGACCTGTGATGCTTCACT 600
Db 578 CTGCGCAATGTGACTGCTATTTATTTTATTCAGATGACAGACCTGTGATGCTTCACT 637
Qy 601 ATACTGCTGTGAGGAGGAAATGCAATACTTTGTTAGGAGGAGGATTGCAAGCTGCAT 660
Db 638 ATACTGCTGTGAGGAGGAAATGCAATACTTTGTTAGGAGGAGGATTGCAAGCTGCAT 697
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAAGAAAGATGCGCAAGCTTGCCTTGGCCAGTAGAATCC 720
Db 698 GTGCAAAAGCTTTGAAAAAGAAAAGAAAGATGCGCAAGCTTGCCTTGGCCAGTAGAATCC 757
Qy 721 GGAATATTCGGAAGAAAGCAATTTTAAACATTTCTTAATATGTCATTTGTGTCTTATG 780
Db 758 GGAATATTCGGAAGAAAGCAATTTTAAACATTTCTTAATATGTCATTTGTGTCTTATG 817
Qy 781 GCTATTTGCTTATGTTGTTGATCTGAAGAAATATATGACGATGAGAAACAATCA 840
Db 818 GCTATTTGCTTATGTTGTTGATCTGAAGAAATATATGACGATGAGAAACAATCA 877
Qy 841 TTGGTATTTATTCACAGTTTATTTATTAACAAGTCACTTTTCAAAAATTTGGATTTT 900
Db 878 TTGGTATTTATTCACAGTTTATTTATTAACAAGTCACTTTTCAAAAATTTGGATTTT 937
Qy 901 TTTATATATTAAGTACTGCTATTCAAATGTGAGTCTACCAATTTTAAATTTATGTTCAAC 960
Db 938 TTTATATATTAAGTACTGCTATTCAAATGTGAGTCTACCAATTTTAAATTTATGTTCAAC 997
Qy 961 TGTGTGAGAGCTGAATTC 979
Db 998 TGTGTGAGAGCTGAATTC 1016

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RESULT 5  
ADL45772  
ID ADL45772 standard; DNA; 2407 BP.

XX ADL45772;  
XX 20-MAY-2004 (first entry)  
XX Human ovarian cancer DNA marker #19662.  
XX Human; ovarian cancer; ds; tumour; cytosolic; DNA marker.  
XX Homo sapiens.  
XX WO200170979-A2.  
XX 27-SEP-2001.  
XX 21-MAR-2001; 2001WO-US009126.  
XX

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PR 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Lee J, Little J;
XX WPI; 2001-611502/70.
XX
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
XX cancer cells as compared to their normal non-cancerous ovarian cells are
XX used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure; SEQ ID NO 19662; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.
XX
XX Sequence 2407 BP; 719 A; 492 C; 474 G; 722 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 979; DB 5; Length 2407;
XX Best Local Similarity 100.0%; Pred. No. 2e-257;
XX Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGACGCTTGGCCAGCGGAGCGCCGACCCCTTGACACGAGACCCGCTGCCCCCTGG 60
Db 74 GGACGCTTGGCCAGCGGAGCGCCGACCCCTTGACACGAGACCCGCTGCCCCCTGG 133
Qy 61 GGGCTGTGATCTGTGCTTTTCTGAGAGGAGCTGCACTGGGGGAGCTGCAAGAGC 120
Db 134 GGGCTGTGATCTGTGCTTTTCTGAGAGGAGCTGCACTGGGGGAGCTGCAAGAGC 193
Qy 121 CAACAGAAATTAAGCGGAGATGTGCTCTGCCCCCTGAGCTAAGAGACCTGCGGGGCC 180
Db 194 CAACAGAAATTAAGCGGAGATGTGCTCTGCCCCCTGAGCTAAGAGACCTGCGGGGCC 253
Qy 181 TACTTCTCGTTACTACTAGACAGGTACAGCGAGAGCTGCGCGCAAGTTCTGTAGGGGG 240
Db 254 TACTTCTCGTTACTACTAGACAGGTACAGCGAGAGCTGCGCGCAAGTTCTGTAGGGGG 313

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QY 241 GGTGGAGGCGCAACGCAATTTCTACACCTGGAGGCTTCCGACGATGCTTCTGTA 300  
 DB 314 GCTGGAGGCGCAACGCAATTTCTACACCTGGAGGCTTCCGACGATGCTTCTGTA 373  
 QY 301 GGAATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTAGTGAGTGGACGACGATGAGG 360  
 DB 374 GGAATGAAAAAGTTCCCAAGTTTCCGGCTGCAAGTAGTGAGTGGACGACGATGAGG 433  
 QY 361 GGTCCAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 420  
 DB 434 GGTCCAGAAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 493  
 QY 421 GTGGGTTCACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAACTACTTGTATGGCT 480  
 DB 494 GTGGGTTCACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAACTACTTGTATGGCT 553  
 QY 481 TCTGGGACCAAGAAAAATTCATGATTTTGTACAGTCCAAAAATGAGGGGACGTGCT 540  
 DB 554 TCTGGGACCAAGAAAAATTCATGATTTTGTACAGTCCAAAAATGAGGGGACGTGCT 613  
 QY 541 CTGCCAATGTGACTGCTATTAATTTTAAATCCAGATACAGACCTGTGATGCTTTCACCT 600  
 DB 614 CTGCCAATGTGACTGCTATTAATTTTAAATCCAGATACAGACCTGTGATGCTTTCACCT 673  
 QY 601 ATACTGCTGTGAGGAGGAAATGACATTAATCTTTGACGAGGAGATTTGCAACGCTGAT 660  
 DB 674 ATACTGCTGTGAGGAGGAAATGACATTAATCTTTGACGAGGAGATTTGCAACGCTGAT 733  
 QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCAAGGCTTGTGCAATGATGATCC 720  
 DB 734 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCAAGGCTTGTGCAATGATGATCC 793  
 QY 721 GGAATAATTCGAAAGAAAGCAATTTTAAACATTTTAAATGTCATCTTGTGCTTTATG 780  
 DB 794 GGAATAATTCGAAAGAAAGCAATTTTAAACATTTTAAATGTCATCTTGTGCTTTATG 853  
 QY 781 GCTTATTTGCTTTATGCTGATGTCGAAGATATATGACGATGAGGAAACAAATCA 840  
 DB 854 GCTTATTTGCTTTATGCTGATGTCGAAGATATATGACGATGAGGAAACAAATCA 913  
 QY 841 TTGGGATTTATTCACGATTTTATTAATACAGTCACTTTTCAAAAAATTTGATTTT 900  
 DB 914 TTGGGATTTATTCACGATTTTATTAATACAGTCACTTTTCAAAAAATTTGATTTT 973  
 QY 901 TTTATATATTAATCTAGCTGCTATTAATGATGAGTCTACCATTTTATTTATGTTCAAC 960  
 DB 974 TTTATATATTAATCTAGCTGCTATTAATGATGAGTCTACCATTTTATTTATGTTCAAC 1033  
 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 1034 TGTTTGTGAGACTGAATTC 1052  
 RESULT 6  
 ABX63609  
 ID ABX63609 standard; cDNA, 2540 BP.  
 AC ABX63609;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Human cDNA #609 differentially expressed in activated vascular tissue.  
 XX  
 KW Human; gene; ss; vascular tissue; cytosolic; atherosclerosis; cardiac; hypotensive; antidiabetic; gynaecological; vasodilator; cerebroprotective; KW hypertensive; diabetes; pre-eclampsia; cancer; coronary; artery disease; KW ischaemia-reperfusion injury; stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002137081-A1.  
 XX

PD 26-SEP-2002.  
 XX  
 PF 08-JAN-2002; 2002US-00044090.  
 XX  
 PR 28-JUL-2000; 2000US-0222469P.  
 PR 08-JAN-2001; 2001US-0260483P.  
 XX  
 PA (BAND/) BANDMAN O.  
 XX  
 PI Bandman O;  
 DR WPI, 2003-110597/10.  
 XX  
 PT Combination for diagnosing, staging, treating, or monitoring the PT progression of treatment of a vascular disease, e.g. atherosclerosis, PT comprises several cDNAs that are differentially expressed in activated PT vascular tissue.  
 XX  
 PS Claim 1, Page: 18pp, English.  
 XX  
 CC This invention relates to a combination comprising several cDNAs that are CC differentially expressed in activated vascular tissue. The invention also CC discloses a high throughput method for detecting differentially expressed CC cDNAs in a sample. The cDNAs of the invention may have CC antiarteriosclerotic; cytosolic; cardiac; hypotensive; antidiabetic; CC gynaecological; vasodilator and cerebroprotective activities and may be CC used in gene therapy. The cDNAs of the invention may be used in a high- CC throughput methods for detecting differential expression of one or more CC cDNAs in a sample, or screening several molecules or compounds to CC identify a molecule or compound that specifically binds a cDNA of the CC invention. A protein encoded by the cDNA may be used to screen several CC molecules or compounds to identify a ligand that specifically binds to CC the protein, or to produce or purify an antibody to the protein that can CC be used to detect a protein in a sample or purify a natural or CC recombinant protein from a sample. The nucleotides may be useful for CC diagnosing, staging, treating or monitoring the progression of treatment CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale CC genetic or gene expression analysis of several new nucleic acid CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for CC diagnosing pre-pathologic disorders, and chronic or acute diseases CC associated with abnormalities in the expression, amount or distribution CC of the protein. The present sequence represents a cDNA of the invention CC that is differentially expressed in activated vascular tissue. Note: The CC sequence data for this patent did not form part of the specification, but CC was obtained in electronic format directly from USPTO at CC <http://seqdata.uspto.gov/sequence.html?docid=20020137081>  
 XX  
 SQ Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 979; DB 8; Length 2540;  
 Best Local Similarity 100.0%; Pred. No. 2e-257;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGAGCGCTTGGCCAGCGGCGGCCGACCCCTGACACCATGAGACCCGCTGCCCTTGG 60  
 DB 27 GGAAGCGCTTGGCCAGCGGCGGCCGACCCCTGACACCATGAGACCCGCTGCCCTTGG 86  
 QY 61 GGCTGTGATTTCTGCTCTTTTCTTGAACGAGGCTGACATGGGGGAGTCTCAAGAGC 120  
 DB 87 GGCTGTGATTTCTGCTCTTTTCTTGAACGAGGCTGACATGGGGGAGTCTCAAGAGC 146  
 QY 121 CAACAGAAATTAACGCGAGATCTGTCTCCGCCCCTAGACTAGAGACCTGCGCGGCCC 180  
 DB 147 CAACAGAAATTAACGCGAGATCTGTCTCCGCCCCTAGACTAGAGACCTGCGCGGCCC 206  
 QY 181 TACTTCTCCGTTACTAGACAGGTACACGACGACCTGCGCGGCTGTACGGGAG 240  
 DB 207 TACTTCTCCGTTACTAGACAGGTACACGACGACCTGCGCGGCTGTACGGGAG 266  
 QY 241 GCTGCGAGGCGAAGCCAAATTTCTACACCTGGAGGCTTGGAGAGATGCTTGTGCGA 300

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Db 267 GCTGCGAGGGCAACGCCAACATTTCTACACCTGGAGGGCTTGACAGATGCTTCTGGA 326
Qy 301 GATGAGAAAAAGTTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACCAACGATGAGG 360
Db 327 GATGAGAAAAAGTTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACCAACGATGAGG 386
Qy 361 GGTCCAGAAAAAGTATTTCTTAATCTTAAGTTCAGATGATGAAAAATCTTTTCG 420
Db 387 GGTCCAGAAAAAGTATTTCTTAATCTTAAGTTCAGATGATGAAAAATCTTTTCG 446
Qy 421 GTGGGTGTCAACCGGAACCGGATGAGAACAGGTTTCCAGATGACCTAATTGATGGCT 480
Db 447 GTGGGTGTCAACCGGAACCGGATGAGAACAGGTTTCCAGATGACCTAATTGATGGCT 506
Qy 481 TCTGGGCAACCAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGACCTGTCT 540
Db 507 TCTGGGCAACCAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGACCTGTCT 566
Qy 541 CTGCGAATGTGACTGCTATTTATTTAATCCAAAGATGACCAAGCTGTGATGCTTCACT 600
Db 567 CTGCGAATGTGACTGCTATTTATTTAATCCAAAGATGACCAAGCTGTGATGCTTCACT 626
Qy 601 ATACTGCTGTGAGGAGGAAATGCAATTAATCTTTAGCAGGAGGATTCGCAACGTCAT 660
Db 627 ATACTGCTGTGAGGAGGAAATGCAATTAATCTTTAGCAGGAGGATTCGCAACGTCAT 686
Qy 661 GTGCAAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTTGCTTGCAGTAAATCC 720
Db 687 GTGCAAAAAGCTTTGAAAAAGAAAAAGAGATCCCAAGCTTTGCTTGCAGTAAATCC 746
Qy 721 GGAANAATCGGAAGAGCAATTTTAAACATCTTAATATGTCATCTGTTGCTTTTANG 780
Db 747 GGAANAATCGGAAGAGCAATTTTAAACATCTTAATATGTCATCTGTTGCTTTTANG 806
Qy 781 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAAACAATCA 840
Db 807 GCTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAAACAATCA 866
Qy 841 TTGGTGATTTATTCACAGTTTATTTAATATACAGTCACTTTTCAAAAATTTGATTTT 900
Db 867 TTGGTGATTTATTCACAGTTTATTTAATATACAGTCACTTTTCAAAAATTTGATTTT 926
Qy 901 TTTATATATTAAGTCTGATTTCAAAATGATGATGATGATTTTATTTATGTTCAAC 960
Db 927 TTTATATATTAAGTCTGATTTCAAAATGATGATGATGATTTTATTTATGTTCAAC 986
Qy 961 TGTTTGTGAGACTGAATTC 979
Db 987 TGTTTGTGAGACTGAATTC 1005

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RESULT 7  
ADJ56337  
ID ADJ56337 standard; cDNA; 2540 BP.

AC ADJ56337;  
XX  
DT 06-MAY-2004 (first entry)  
DE Human cDNA differentially expressed in MYCN activated cells Segid 143.  
XX  
KM human; differential expression; transactivator; proto-oncogene;  
KM neuroblastoma; small cell lung cancer; cytotoxic; gene therapy; ss;  
XX MYCN activated cell.  
OS Homo sapiens.  
XX  
PN US2003119009-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 25-FEB-2002; 2002US-00084817.  
XX

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PR 23-FEB-2001; 2001US-0270784P.
XX
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLON/) PLON S B.
PA (SHOH/) SHOHER J M.
XX
PI Stuart SG, Nuchtern JG, Plon SB, Shoher JM;
XX
DR WPI: 2003-635698/60.
XX
PT New genes regulated by MYCN activation, useful in gene therapy,
PT particularly for treating a subject with e.g. neuroblastoma or other
PT cancers, or for diagnosing, staging or monitoring the treatment of the
PT cancer.
XX
PS Claim 1; SEQ ID NO 143; 27bp; English.
XX
CC This invention relates to novel isolated cDNAs that are differentially
CC expressed in MYCN activated cells. Specifically, it refers to
CC polynucleotide sequences that exhibit differential expression patterns in
CC cells activated by the transactivator MYCN, where MYCN is a proto-
CC oncogene that is amplified in neuroblastoma cells and is common in small
CC cell lung cancers. The present invention describes these cDNA molecules
CC as useful for in hybridisation assays to detect expression of nucleic
CC acids (or complementary nucleic acids) in a present in a given sample, as
CC well as for screening assays by identifying molecules or compounds that
CC specifically bind the cDNA as a ligand and modulate function or activity.
CC Accordingly, these compositions exhibit cytotoxic activity and can also
CC be used for gene therapy purposes. This polynucleotide sequence is a cDNA
CC that is differentially expressed in MYCN activated cells, given in an
CC exemplification of the invention. NOTE: This sequence does not appear in
CC the printed specification but has been obtained in electronic format from
CC the US Patent Office at
CC ftp://seqdata.uspto.gov/sequence.html?docid=20030119009.
XX
SQ Sequence 2540 BP; 806 A; 458 C; 534 G; 742 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 979; DB 10; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 26-257;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 GAGAGCCCTTGGCCAGCGGCGCGCCGACCCCTGACCATGAGACCCGCTGCGCCCTG 60
Db 27 GAGAGCCCTTGGCCAGCGGCGCGCCGACCCCTGACCATGAGACCCGCTGCGCCCTG 86
Qy 61 GAGCTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTCAAGAC 120
Db 87 GAGCTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTGTGAGAC 146
Qy 121 CAACAGAAATTAAGCGCGAGATCTGTCTCTGCTGCTTGAATGACGACCTTGGCGGCC 180
Db 147 CAACAGAAATTAAGCGCGAGATCTGTCTCTGCTGCTTGAATGACGACCTTGGCGGCC 206
Qy 181 TACTTCTCGTTACTACTACAGACGATGATGATGATGATGATGATGATGATGATGATG 240
Db 207 TACTTCTCGTTACTACTACAGACGATGATGATGATGATGATGATGATGATGATGATG 266
Qy 241 GCTGCGAGGGCAACGCCCAATTTCTACACCTGAGAGCTTTCGACGATGCTTCTGGA 300
Db 267 GCTGCGAGGGCAACGCCCAATTTCTACACCTGAGAGCTTTCGACGATGCTTCTGGA 326
Qy 301 GATGAGAAAAAGTTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACCAACGATGAGG 360
Db 327 GATGAGAAAAAGTTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAACCAACGATGAGG 386
Qy 361 GGTCCAGAAAAAGTATTTCTTAATCTTAAGTTCAGATGATGAAAAATCTTTTCG 420
Db 387 GGTCCAGAAAAAGTATTTCTTAATCTTAAGTTCAGATGATGAAAAATCTTTTCG 446
Qy 421 GTGGGTGTCAACCGGAACCGGATGAGAACAGGTTTCCAGATGACCTAATTGATGGCT 480
Db 447 GTGGGTGTCAACCGGAACCGGATGAGAACAGGTTTCCAGATGACCTAATTGATGGCT 506

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QY 481 TCTGGCAGCAAGAAATTCATCTTTTGTCTACGTCGCAAAAGTAGGAGCTGTGCT 540  
 DB 507 TCTGGCAGCAAGAAATTCATCTTTTGTCTACGTCGCAAAAGTAGGAGCTGTGCT 566  
 QY 541 CTGGCAATGTGACTGCTATTTATTTATTCAGAGATAGAGAACTGTGATGCTTCAACCT 600  
 DB 567 CTGGCAATGTGACTGCTATTTATTTATTCAGAGATAGAGAACTGTGATGCTTCAACCT 626  
 QY 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTTGTAGCAGGAGATGCAACGTCAT 660  
 DB 627 ATACTGCTGTGAGGAGAAATGACATTAATCTTTGTAGCAGGAGATGCAACGTCAT 686  
 QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTGGCTTGGCAATGACT 720  
 DB 687 GTGCAAAAGCTTTGAAAAAGAAAAAGAAATGCCAAAGCTTGGCTTGGCAATGACT 746  
 QY 721 GGAATAATGGAAGAAAGCAATTTTAAACATCTTAATATGTCATCTGTTGCTTTATG 780  
 DB 747 GGAATAATGGAAGAAAGCAATTTTAAACATCTTAATATGTCATCTGTTGCTTTATG 806  
 QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 840  
 DB 807 GCTTATTTGCTTTATGTTGTTATCTGAAGAAATATATGACAGATGAGAAACAAATCA 866  
 QY 841 TTGGTGATTTATTCACCACTTTTATTTATTAACAGTCACTTTTCAAAATTTGATTTT 900  
 DB 867 TTGGTGATTTATTCACCACTTTTATTTATTAACAGTCACTTTTCAAAATTTGATTTT 926  
 QY 901 TTTATATATTAATTAATCTGCTATTTCAAAATGAGTCACTTTTATTAATTTATGTTCAAC 960  
 DB 927 TTTATATATTAATTAATCTGCTATTTCAAAATGAGTCACTTTTATTAATTTATGTTCAAC 986  
 QY 961 TGTGTTGTGAGACTGAATTC 979  
 DB 987 TGTGTTGTGAGACTGAATTC 1005

RESULT 8  
 ADS19178 standard; cDNA, 1141 BP.

AC ADS19178;  
 XX 16-DEC-2004 (first entry)  
 DT Human tissue factor pathway inhibitor 2 cDNA, SEQ ID NO:19.  
 XX  
 DB Human tissue factor pathway inhibitor 2 cDNA, SEQ ID NO:19.  
 XX  
 KW Mesenchymal stem cell; marker gene; serine protease inhibitor;  
 KW cysteine protease inhibitor; adrenomedullin; apolipoprotein D;  
 KW collagen type XV alpha 1; CUG triplet repeat RNA binding protein;  
 KW dermatopontin; isocitrate dehydrogenase 2;  
 KW major histocompatibility complex class II; MHC class II; DR beta 3;  
 KW DR alpha; protein tyrosine kinase 7; Same8-like phosphotyrosine protein;  
 KW C-type lectin superfamily member 2; matrix metalloprotease 1;  
 KW tissue factor pathway inhibitor 2; microarray; DNA chip; detection;  
 KW identification; human; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO2004081174-A2.  
 XX  
 PD 23-SEP-2004.  
 XX  
 PF 27-FEB-2004; 2004MO-JP002457.  
 XX  
 PR 10-MAR-2003; 2003JP-00063077.  
 XX  
 PA (MISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
 PA (TWO-) TWO CELLS CO LTD.  
 PA (KATO/) KATO Y.  
 XX  
 XX Kato Y, Tsuji K, Koike C;  
 PI

XX WPI, 2004-699450/68.  
 DR GENBANK, AL550357.  
 XX  
 PT New gene markers e.g. serine or cysteine protease inhibitor gene, major  
 PT histocompatibility complex class II gene specific for mesenchymal stem  
 PT cells, useful for detecting and identifying mesenchymal stem cells.  
 XX  
 PS Claim 1; SEQ ID NO 19; 171bp; Japanese.  
 XX  
 CC The invention relates to marker genes for detecting mesenchymal stem  
 CC cells, selected from approximately 145 genes. The mesenchymal stem cell  
 CC marker genes include the serine (or cysteine) protease inhibitor gene  
 CC (ADS19160), the adrenomedullin gene (ADS19161), the apolipoprotein D gene  
 CC (ADS19163), the collagen type XV alpha 1 gene (ADS19165), the CUG triplet  
 CC repeat RNA binding protein 2 gene (ADS19166), the dermatopontin gene  
 CC (ADS19168), the isocitrate dehydrogenase 2 gene (ADS19169), the major  
 CC histocompatibility complex class II DR beta 3 or DR alpha genes (ADS19170  
 CC and ADS19205, respectively), the protein tyrosine kinase 7 gene  
 CC (ADS19171), the Same8-like phosphotyrosine protein (ADS19173), the C-type  
 CC lectin superfamily member 2 gene (ADS19174), the matrix metalloprotease 1  
 CC gene (ADS19176), and the tissue factor pathway inhibitor 2 gene  
 CC (ADS19178). The invention also relates to marker gene-specific probes and  
 CC microarrays or DNA chips comprising such probes; reverse transcription-  
 CC PCR (RT-PCR) and real-time PCR primers specific for marker genes of the  
 CC invention (ADS19179-ADS19204 and ADS19206-ADS19275); mesenchymal stem  
 CC cell polypeptide markers (ADS19162, ADS19164, ADS19167, ADS19172,  
 CC ADS19175 and ADS19177) and antibodies specific for them; and kits  
 CC comprising probe microarrays or antibodies for identifying mesenchymal  
 CC stem cells. The marker genes and polypeptides, probe microarrays, primers  
 CC and antibodies permit easy and reliable detection and identification of  
 CC mesenchymal stem cells, e.g., by determining the expression level of a  
 CC marker gene and subsequently performing Northern blot analysis. The  
 CC present sequence represents a specifically claimed human tissue factor  
 CC pathway inhibitor 2 cDNA.  
 XX  
 SQ Sequence 1141 BP; 317 A; 246 C; 259 G; 319 T; 0 U; 0 Other;

Query Match 99.8%; Score 977.4; DB 13; Length 1141;  
 Best Local Similarity 99.9%; Pred. No. 3.7e-257;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGGCCAGCGGCGCCGAGACCCCTGACACATGAGACCCGCTGCCCCCTGG 60  
 DB 18 GAGCGCCTTGGCCAGCGGCGCCGAGACCCCTGACACATGAGACCCGCTGCCCCCTGG 77  
 QY 61 GGCTGTGATTTCTGCTGCTTTTCCGACGAGGCTGCACTGGGAGATCTGCTGAGAGC 120  
 DB 78 GGCTGTGATTTCTGCTGCTTTTCCGACGAGGCTGCACTGGGAGATCTGCTGAGAGC 137  
 QY 121 CAACAGAAATTAACGCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGGGGCC 180  
 DB 138 CAACAGAAATTAACGCGAGATCTGCTCTGCCCCCTAGACTAGAGACCTGCGGGGCC 197  
 QY 181 TACTTTCCTGTTACTACTACACAGGTRACAGCAGAGTGCCTGCTTCTGTRACGGGG 240  
 DB 198 TACTTTCCTGTTACTACTACACAGGTRACAGCAGAGTGCCTGCTTCTGTRACGGGG 257  
 QY 241 GCTGCGAGGGCAACGCAACATTTCTACACTGAGGAGCTTGGGAGAGATGCTTGGTGG 300  
 DB 258 GCTGCGAGGGCAACGCAACATTTCTACACTGAGGAGCTTGGGAGAGATGCTTGGTGG 317  
 QY 301 GGATGAAAAAGTCCCAAGTTTGCAGGCTGCAAGTGAAGTGGAGACGACGATGTGAGG 360  
 DB 318 GGATGAAAAAGTCCCAAGTTTGCAGGCTGCAAGTGAAGTGGAGACGACGATGTGAGG 377  
 QY 361 GGTCCACGAAAAATATTTCTTTATCTAAGTTCATGACATGTGAAAAATCTTTTCCG 420  
 DB 378 GGTCCACGAAAAATATTTCTTTATCTAAGTTCATGACATGTGAAAAATCTTTTCCG 437  
 QY 421 GTGGGTGACCCGGAAACCGGATTGAGAACAGGTTTCCAGANGAGCTACTGTATGAGGCT 480  
 DB 438 GTGGGTGACCCGGAAACCGGATTGAGAACAGGTTTCCAGANGAGCTACTGTATGAGGCT 497



QY 481 TCTGGCAACCAAGAAATTCATGATTTTGCTAGTCACCAAGATGAGGACCTGCT 540  
 DB 498 TCTGGCAACCAAGAAATTCATGATTTTGCTAGTCACCAAGATGAGGACCTGCT 557  
 QY 541 CTGCAATGTCATGCTGCTATTATTTAAATCCAGATGAGAACTGTATGCTTCACT 600  
 DB 558 CTGCAATGTCATGCTGCTATTATTTAAATCCAGATGAGAACTGTATGCTTCACT 617  
 QY 601 ATACTGCTGTGAGAGGAAATGCAATTAATCTTTGAGCAGGAGATTCAGAACTGCAT 660  
 DB 618 ATACTGCTGTGAGAGGAAATGCAATTAATCTTTGAGCAGGAGATTCAGAACTGCAT 677  
 QY 661 GTGCAAAAGCTTTGAAAAAGAAAGAGCCCAAGCTTCCCTTCCCACTAATCC 720  
 DB 678 GTGCAAAAGCTTTGAAAAAGAAAGAGCCCAAGCTTCCCTTCCCACTAATCC 737  
 QY 721 GGAATATTCGGAAGAGCAATTTTAAATCTTAATATGTCATCTGTGCTTTTANG 780  
 DB 738 GGAATATTCGGAAGAGCAATTTTAAATCTTAATATGTCATCTGTGCTTTTANG 797  
 QY 781 GCTATTTGCTTTATGTTGTTATGTAAGATTAATATGACAGATGAGAAACAAATCA 840  
 DB 798 GCTATTTGCTTTATGTTGTTATGTAAGATTAATATGACAGATGAGAAACAAATCA 857  
 QY 841 TTGGGATTTATTCACCACTTTTATTAATATGACATCTTTTCAAAAATTTGATTT 900  
 DB 858 TTGGGATTTATTCACCACTTTTATTAATATGACATCTTTTCAAAAATTTGATTT 917  
 QY 901 TTTATATTAATCTAGCTGCTATTTCAATATGAGTCTACATTTTAAATTAATGTTTAC 960  
 DB 918 TTTATATTAATCTAGCTGCTATTTCAATATGAGTCTACATTTTAAATTAATGTTTAC 977  
 QY 961 TGTGTTGAGACTGAATTC 979  
 DB 978 TGTGTTGAGACTGAATTC 996

## RESULT 9

AB876528 standard, cDNA, 1142 BP.

AB876528;

11-DEC-2002 (first entry)

CDNA encoding human ovarian cancer marker M588.

Human, ovarian cancer, marker; cancer; familial history; brain disorder;  
 central nervous system disorder; bacterial meningitis; viral meningitis;  
 Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;  
 brain herniation; inflammation; encephalitis; testicular disorder;  
 nonuberculous granulomatous orchitis; connective tissue disorder;  
 heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;  
 histological type: carcinogenic; ovarian cancer marker; gene; ss.

Homo sapiens.

MO200271928-A2.

19-SEP-2002.

14-MAR-2002, 2002MO-US007826.

14-MAR-2001, 2001US-0276025P.

14-MAR-2001, 2001US-0276026P.

10-AUG-2001, 2001US-0311732P.

19-SEP-2001, 2001US-0323580P.

26-SEP-2001, 2001US-0324967P.

26-SEP-2001, 2001US-0325102P.

26-SEP-2001, 2001US-0325149P.

XX Monahan JE, Gannavarapu M, Hoersch S, Kamath S, Kovatis SG;  
 PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vieley FO, Mills GB;  
 PI Baet RC, Lu K, Schmandt RE, Zhao X, Glatt K;  
 DR WPI, 2002-723277/78.  
 XX P-PSDB, ABG96429.  
 PT Assessing whether a patient is afflicted with ovarian cancer, useful in  
 PT assessing the stage or progression of the disease, comprises comparing  
 PT the expression level of a cancer marker in a sample from a patient and  
 PT from a non cancer patient.  
 XX  
 PS Disclosure: Page 437; 481pp; English.  
 XX The present invention relates to a new method for assessing whether a  
 CC patient is afflicted with ovarian cancer. The method involves comparing  
 CC the expression level of a marker in a patient sample and the normal level  
 CC of expression of the marker in a control non-ovarian cancer sample, where  
 CC the marker is selected from 363 cancer markers described in the  
 CC specification. The method of the invention is useful in diagnosing or  
 CC characterizing cancer, in detecting the presence of cancer as early as  
 CC possible, and the recurrence of ovarian cancer. The method may also be of  
 CC particular use with patients having an enhanced risk of developing  
 CC ovarian cancer (e.g. patients having a familial history of ovarian  
 CC cancer). The cancer markers may be used in the management and treatment  
 CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
 CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain  
 CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),  
 CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
 CC testicular disorders (e.g. nonuberculous granulomatous orchitis),  
 CC connective tissue disorders, or heart disorders (e.g. ischaemic heart  
 CC disease or atherosclerosis). The compositions and methods may also be  
 CC used in assessing the histological type of neoplasm associated with  
 CC ovarian cancer, monitoring the progression of ovarian cancer, determining  
 CC whether ovarian cancer has metastasized or is likely to metastasize,  
 CC selecting a composition for inhibiting ovarian cancer, assessing the  
 CC ovarian carcinogenic potential of a compound, or inhibiting ovarian  
 CC cancer or at risk of developing ovarian cancer. The present nucleic acid  
 CC sequence encodes one of the ovarian cancer markers described in the  
 CC invention  
 CC  
 SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
 Query Match 99.3%; Score 972.2; DB 6; Length 1142;  
 Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
 Matches 974; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGAAGCTTGGCCAGAGCGGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTGG 60  
 DB 19 GAGAGCTTGGCCAGAGCGGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTGG 78  
 QY 61 GAGCTGCAATTCGCTGCTTTTCCGACGAGGCTGCACTGGGCGATGCTGCTGAGAGC 120  
 DB 79 GAGCTGCAATTCGCTGCTTTTCCGACGAGGCTGCACTGGGCGATGCTGCTGAGAGC 138  
 QY 121 CAACGAAATPAGCGGAGATCTGCTCTGCCCCCTGACTAGAGCACTTCCGCGGCC 180  
 DB 139 CAACGAAATPAGCGGAGATCTGCTCTGCCCCCTGACTAGAGCACTTCCGCGGCC 198  
 QY 181 TACTTCTCGTTACTACAGACAGGTACAGGAGCTGCGCGAGTCCGTTACGAGGG 240  
 DB 199 TACTTCTCGTTACTACAGACAGGTACAGGAGCTGCGCGAGTCCGTTACGAGGG 258  
 QY 241 GCTGCGAGGCAAGCCCAATTTCTTCACTGAGAGCTTGGCGATGCTTGGCTGGA 300  
 DB 259 GCTGCGAGGCAAGCCCAATTTCTTCACTGAGAGCTTGGCGATGCTTGGCTGGA 318  
 QY 301 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTAGG 360  
 DB 319 GGAATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTAGG 378  
 QY 361 GGTCCAGAGAAAGTAATTTCTTTAATCTAAGTTCATGACATGAGAAATTTCTTTCCG 420

DB 379 GGTTCACGAAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAAAATTCCTTTCCG 438  
OY 421 GTGGGTGTCAACCGGAACGGATTTGAGAACAGGTTTCCAGATTAAGCTACTTGATGGCT 480  
DB 439 GTGGGTGTCAACCGGAACGGATTTGAGAACAGGTTTCCAGATTAAGCTACTTGATGGCT 498  
OY 481 TCTGCGCACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 499 TCTGCGCACCAAGAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 558  
OY 541 CTGCCAATGTGACTGCTGATTTATTTATTCAGATGAGGAGCTGTGATGCTTCACT 600  
DB 559 CTGCCAATGTGACTGCTGATTTATTTATTCAGATGAGGAGCTGTGATGCTTCACT 618  
OY 601 ATACTGCTGTGAGGAGGATGACAAATACTTGTAGCAGGAGGATTTGCAAACTGTGAT 660  
DB 619 ATACTGCTGTGAGGAGGATGACAAATACTTGTAGCAGGAGGATTTGCAAACTGTGAT 678  
OY 661 GTGCAGAAAGCTTTGAAAAAGAAAAGAAAGATGCCAAAGCTTGTGCTCCAGTAGAATCC 720  
DB 679 GTGCAGAAAGCTTTGAAAAAGAAAAGAAAGATGCCAAAGCTTGTGCTCCAGTAGAATCC 738  
OY 721 GGAATAATTCGAAAGAGCAATTTTAACATCTTAAATGTCATCTTGTGCTTTATG 780  
DB 739 GGAATAATTCGAAAGAGCAATTTTAACATCTTAAATGTCATCTTGTGCTTTATG 798  
OY 781 GCTTATTTGCTTTATGTTGATCTGAGAAATATATATGACAGATGAGAAACAAATCA 840  
DB 799 GCTTATTTGCTTTATGTTGATCTGAGAAATATATATGACAGATGAGAAACAAATCA 858  
OY 841 TTGGTGAATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTT 900  
DB 859 TTGGTGAATTTATTCACCAAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTT 918  
OY 901 TTTAATATTAATCTAGCTGCTATTCAAATGATGATGATCACTTTTAAATTTAGTTTCAAC 960  
DB 919 TTTAATATTAATCTAGCTGCTATTCAAATGATGATGATCACTTTTAAATTTAGTTTCAAC 978  
OY 961 TGTGTGTGAGACTGAT 977  
DB 979 TGTGTGTGAGACTGAT 995

RESULT 10  
ID ABX76328 standard; DNA; 1142 BP.  
AC ABX76328;  
XX  
XX 02-APR-2003 (first entry)  
DE  
XX Lung cancer-associated polynucleotide #192.  
XX  
XX Lung cancer-associated polynucleotide; gene; de; cytostatic; emphysema;  
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
XX small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
XX chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
XX interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
XX  
XX unidentified.  
OS  
XX  
XX WO200286443-A2.  
XX  
XX 31-OCT-2002.  
PD  
XX  
XX 18-APR-2002; 2002WO-US012476.  
PF  
XX 18-APR-2001; 2001US-0284770P.  
PR 10-MAY-2001; 2001US-0290492P.  
PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.  
XX  
XX (BOSB-) BOS BIOTECHNOLOGY INC.  
XX  
XX Aziz N, Murray R;  
XX WPI; 2003-093161/08.  
DR P-PSDB; ABUS65599.  
XX  
XX Detecting a lung cancer-associated transcript in a cell from a patient  
PT for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased  
PT expression in lung cancer.  
XX  
XX  
PS Claim 22; Page 332-333; 453pp; English.  
XX  
XX The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung cancer-  
CC associated polynucleotides and polypeptides are used for identifying a  
CC compound that modulates a lung cancer-associated polypeptide, for  
CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
CC cancer in a patient and for treating a mammal having lung cancer by  
CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma, and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the  
CC invention.  
XX  
SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
XX

Query Match 99.3%; Score 972.2; DB 8; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GGACGCTTGGCCAGCGGCGCGCCGACCCCTTGACACATGAGACCCGCTGCCCTTGG 60  
DB 19 GAGCGCTTGGCCAGCGGCGCGCCGACCCCTTGACACATGAGACCCGCTGCCCTTGG 78  
OY 61 GGCTGTGATTCCTGCTGCTTTTCTGACGAGGCTGACCTGCGGAGATGCTGACAGAGC 120  
DB 79 GGCTGTGATTCCTGCTGCTTTTCTGACGAGGCTGACCTGCGGAGATGCTGACAGAGC 138  
OY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGGAGCC 180  
DB 139 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGGAGCC 198  
OY 181 TACTTCTCCGTACTACTAGACAGGTACACGACGAGCTGCGGCAAGTTCTGTACGGGG 240  
DB 199 TACTTCTCCGTACTACTAGACAGGTACACGACGAGCTGCGGCAAGTTCTGTACGGGG 258  
OY 241 GCTGCGAGGGCAAGCAATTTCTACACCTGCGGAGGCTTGTGACGAGATGCTGTGCGA 300  
DB 259 GCTGCGAGGGCAAGCAATTTCTACACCTGCGGAGGCTTGTGACGAGATGCTGTGCGA 318  
OY 301 GGATAGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 360  
DB 319 GGATAGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 378  
OY 361 GGTCCACGAAAGATTTCTTATATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 420  
DB 379 GGTCCACGAAAGATTTCTTATATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 438  
OY 421 GTGGGTGTCAACCGGAACGGATTTGAGAACAGGTTTCCAGATTAAGCTACTTGATGGCT 480  
DB 439 GTGGGTGTCAACCGGAACGGATTTGAGAACAGGTTTCCAGATTAAGCTACTTGATGGCT 498

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OY 481 TCTGGGCAACAAAGAAATTCATCTTGTGCTACAGTCCAAAAGATGAGGGACCTGTCT 540
DB 499 TCTGGGCAACAAAGAAATTCATCTTGTGCTACAGTCCAAAAGATGAGGGACCTGTCT 558
OY 541 CTGCCAATGTGACTGCTGCTATTTATTTAATCCAAAGATACAGAACTGTGATCTTCACT 600
DB 559 CTGCCAATGTGACTGCTGCTATTTAATTTAATCCAAAGATACAGAACTGTGATCTTCACT 618
OY 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGGATTCGAAACCTGCAT 660
DB 619 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGGATTCGAAACCTGCAT 678
OY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGATGCAAGCTTCGCTTGCAGTAAATCC 720
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGATGCAAGCTTCGCTTGCAGTAAATCC 738
OY 721 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAATAATGTCATCTTGTGTCTTTATG 780
DB 739 GGAATAATCGAAGAAAGCAATTTTAAACATCTTAATAATGTCATCTTGTGTCTTTATG 798
OY 781 GCTTATTTGCTTTAATGTTGTTATCTGAAGATTAATATGACGATGAGGAAACAAATCA 840
DB 799 GCTTATTTGCTTTAATGTTGTTATCTGAAGATTAATATGACGATGAGGAAACAAATCA 858
OY 841 TTGCGATTTATTCACCAAGTTTATTTAATAACAGTCCCTTTGAAAAATTTGATTTT 900
DB 859 TTGCGATTTATTCACCAAGTTTATTTAATAACAGTCCCTTTGAAAAATTTGATTTT 918
OY 901 TTTATATATTAAGTACGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 960
DB 919 TTTATATATTAAGTACGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 978
OY 961 TGTTTGTGAGACTGAAT 977
DB 979 TGTTTGTGAGACTGAAT 995

RESULT 11
ABX08764
ID ABX08764 standard; cDNA, 1142 BP.
AC ABX08764;
XX 21-JAN-2003 (first entry)
DE Angiogenesis-associated human polynucleotide sequence #26.
XX Human; angiogenesis-associated transcript; angiogenesis;
XX angiogenesis-associated disease; cancer; cytostatic; gene therapy; gene;
XX 88.
XX Homo sapiens.
XX OS
XX MO200279492-A2.
XX 10-OCT-2002.
XX 14-FEB-2002; 2002WO-US004915.
XX 14-FEB-2001; 2001US-00784356.
XX 22-FEB-2001; 2001US-00791399.
XX 19-APR-2001; 2001US-0285475P.
XX 03-AUG-2001; 2001US-0310025P.
XX 13-NOV-2001; 2001US-0350666P.
XX 29-NOV-2001; 2001US-0334244P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Murray R, Glynn R, Watson SR, Aziz N,
XX WPI; 2003-040681/03.
XX P-PSDB; ABU03481.
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```
XX Detecting angiogenesis-associated transcript in a cell for diagnosing and
PT treating cancer by contacting a sample with a polynucleotide that
PT exhibits changes in expression level as a function of time in tissue
PT undergoing angiogenesis.
XX
XX Example 2; Page 205; 291pp; English.
XX
XX The present invention relates to methods and compositions for detecting
XX an angiogenesis-associated transcript in a cell in a patient. The method
XX involves contacting a biological sample from the patient with a
XX polynucleotide that selectively hybridizes to a sequence at least 80%
XX identical to any of the angiogenesis-associated human polynucleotide
XX sequences given in the specification. These angiogenesis-associated
XX polynucleotide sequences comprise genes that exhibit changes in
XX expression levels as a function of time in tissue undergoing
XX angiogenesis. The method and the polynucleotide sequences of the
XX invention are useful for diagnosing and treating angiogenesis and
XX angiogenesis-associated diseases e.g. cancer. The polynucleotide
XX sequences are also useful in the gene therapy of such disorders. The
XX angiogenesis-associated proteins encoded by the polynucleotide sequences
XX are useful as a vaccine for therapeutic and prophylactic immunisation.
XX ABX08739-ABX08853 represent angiogenesis-associated polynucleotide
XX sequences
XX
SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;
XX
Query Match 99.3%; Score 972.2; DB 10; Length 1142;
Beat Local Similarity 99.7%; Pred. No. 9.9e-25;
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 GGAAGCCTTGGCCAGCGGCGCGCCGCAACCCCTGACAGTGAACCCGCTGCGCCCTGG 60
DB 19 GAGCGCTTGGCCAGCGGCGCGCCGCAACCCCTGACAGTGAACCCGCTGCGCCCTGG 78
OY 61 GGCTGTGCAATCTGCTGCTTTTCTGACGAGGCTGCACTGGCGANTCTGCTCAGAGC 120
DB 79 GGCTGTGCAATCTGCTGCTTTTCTGACGAGGCTGCACTGGCGANTCTGCTCAGAGC 138
OY 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGGGCC 180
DB 139 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGGGCC 198
OY 181 TACTTCTCCGTACTACAGACAGGTACAGCGAGGCTGCGGAGTCCGTGACGGGG 240
DB 199 TACTTCTCCGTACTACAGACAGGTACAGCGAGGCTGCGGAGTCCGTGACGGGG 258
OY 241 GCTGGAAGGCAACGCAACAATTTCTACCTGGGAGGCTTGCAGAGTCTTCTGGA 300
DB 259 GCTGGAAGGCAACGCAACAATTTCTACCTGGGAGGCTTGCAGAGTCTTCTGGA 318
OY 301 GGATGAAAAAGTTCCAAAGTTTCCGGCTGCAAGTGAATGTGAGCAACAGTGTGAGG 360
DB 319 GGATGAAAAAGTTCCAAAGTTTCCGGCTGCAAGTGAATGTGAGCAACAGTGTGAGG 378
OY 361 GGTCCAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAAATTTCTTCCG 420
DB 379 GGTCCAGAAAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAAATTTCTTCCG 438
OY 421 GTGGGTGTCAACGGAACCGGATTTGAGACAAGTTTCCAGATGAAGCTACTTGTATGGCT 480
DB 439 GTGGGTGTCAACGGAACCGGATTTGAGACAAGTTTCCAGATGAAGCTACTTGTATGGCT 498
OY 481 TCTGGGCAACAAAGAAATTCATCTTGTGCTACAGTCCAAAAGATGAGGGACCTGTCT 540
DB 499 TCTGGGCAACAAAGAAATTCATCTTGTGCTACAGTCCAAAAGATGAGGGACCTGTCT 558
OY 541 CTGCCAATGTGACTGCTGCTATTTAATTTAATCCAAAGATACAGAACTGTGATCTTCACT 600
DB 559 CTGCCAATGTGACTGCTGCTATTTAATTTAATCCAAAGATACAGAACTGTGATCTTCACT 618
OY 601 ATACTGCTGTGAGGAGAAATGACATTAATCTTGTAGCAGGAGGATTCGAAACCTGCAT 660
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Db 619 ATATGGCTGTGAGGAAATGACATTAATCTTTGTCAGGAGGATTCGAAAAGCTGCAT 678  
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGTGCTTGGCAGTAGAATCC 720  
Db 679 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGTGCTTGGCAGTAGAATCC 738  
Qy 721 GGAATAATTCGAAAGACATTTTAACTTCTTAATATGTCATCTGTGTTGCTTTATG 780  
Db 729 GGAATAATTCGAAAGACATTTTAACTTCTTAATATGTCATCTGTGTTGCTTTATG 798  
Qy 781 GCTTATTTGCTTTATGTTGTTATCGAAGATTAATATGACAGATGAGGAAACAAATCA 840  
Db 799 GCTTATTTGCTTTATGTTGTTATCGAAGATTAATATGACAGATGAGGAAACAAATCA 858  
Qy 841 TTGCTGATTTATTCACAGCTTTTATTAATACAGTCATTTTCAAAAATTTGGATTTT 900  
Db 859 TTGGGATTTATTCACAGCTTTTATTAATACAGTCATTTTCAAAAATTTGGATTTT 918  
Qy 901 TTTATATATTAATTAAGTCTGCTATTCAAATGTGAGTCACTATTTTAAATTTATGTTCAAC 960  
Db 919 TTTATATATTAATTAAGTCTGCTATTCAAATGTGAGTCACTATTTTAAATTTATGTTCAAC 978  
Qy 961 TGTGTTGAGACTGAAT 977  
Db 979 TGTGTTGAGACTGAAT 995  
RESULT 12  
ADN38705  
ID ADN38705 standard; cDNA; 1142 BP.  
AC ADN38705;  
XX  
XX 17-JUN-2004 (first entry)  
DT  
XX  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:23.  
XX  
XX Human; differential expression; cancer; angiogenic disorder;  
KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KM inflammatory disease; autoimmune disease;  
KM retinal neovascularization syndrome; scarring; uterine fibroid;  
KM detection; diagnosis; prognosis; drug screening; drug targeting;  
KM wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KM vulnery; gene therapy; vaccine; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003042661-A2.  
PN  
XX  
XX 22-MAY-2003.  
PD  
XX  
XX 13-NOV-2002; 2002WO-US036810.  
PF  
XX  
XX 13-NOV-2001; 2001US-0350666P.  
PR 21-NOV-2001; 2001US-033464P.  
PR 29-NOV-2001; 2001US-0334393P.  
PR 03-DEC-2001; 2001US-0335394P.  
PR 14-DEC-2001; 2001US-0340376P.  
PR 08-JAN-2002; 2002US-0347211P.  
PR 10-JAN-2002; 2002US-0347349P.  
PR 08-FEB-2002; 2002US-0355250P.  
PR 13-FEB-2002; 2002US-0356714P.  
PR 20-FEB-2002; 2002US-0359077P.  
PR 29-MAR-2002; 2002US-036809P.  
PR 04-APR-2002; 2002US-0370110P.  
PR 12-APR-2002; 2002US-0372246P.  
PR 05-JUN-2002; 2002US-038614P.  
PR 16-JUL-2002; 2002US-0396839P.  
PR 22-JUL-2002; 2002US-039775P.  
PR 22-JUL-2002; 2002US-0397845P.  
PR 09-SEP-2002; 2002US-0409450P.  
XX  
XX (BOSB-) EOS BIOTECHNOLOGY INC.  
PA

XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A;  
XX  
XX MPI: 2003-466649/44.  
DR P-PsDB; ADN38706.  
XX  
XX Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.  
XX  
XX  
XX Claim 8; SEQ ID NO 23; 1385bp; English.  
XX  
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularization syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a nucleic acid sequence of the invention.  
XX  
XX Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
SQ  
Query Match 99.3%; Score 972.2; DB 11; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GAGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGACCCGCTGCGCCCTGG 60  
Db 19 GAGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGACCCGCTGCGCCCTGG 78  
Qy 61 GCGTGTGATTTCTGCTGTTTCTTCTGACGAGGCTGCTGCGGAGTCTGTCAGAGC 120  
Db 79 GCGTGTGATTTCTGCTGTTTCTTCTGACGAGGCTGCTGCGGAGTCTGTCAGAGC 138  
Qy 121 CAACAGAAATTAACGCGGAGATCTGCTCTGCGCCCTGACATGACGACCTGCGGGGCC 180  
Db 139 CAACAGAAATTAACGCGGAGATCTGCTCTGCGCCCTGACATGACGACCTGCGGGGCC 198  
Qy 181 TACTTCTCGTTACTACTACAGAGTACAGCAGAGAGTGCAGGTTCTGTACGGGG 240  
Db 199 TACTTCTCGTTACTACTACAGAGTACAGCAGAGAGTGCAGGTTCTGTACGGGG 258  
Qy 241 GCTGAGAGGCAAGCCCAATTTCTACACTGAGAGGCTTGGACAGATCTTCTCTGA 300  
Db 259 GCTGAGAGGCAAGCCCAATTTCTACACTGAGAGGCTTGGACAGATCTTCTCTGA 318  
Qy 301 GGATAGAAAAGTTCCCAAGTTTGGCGGCTGCAAGTGTGTGACAGCAGTGTGAGG 360  
Db 319 GGATAGAAAAGTTCCCAAGTTTGGCGGCTGCAAGTGTGTGACAGCAGTGTGAGG 378  
Qy 361 GGTCCAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTGTGAAAATTTCTTTCCG 420  
Db 379 GGTCCAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTGTGAAAATTTCTTTCCG 438  
Qy 421 GTGGGTGTCACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAAGCTACTGTATGGGCT 480  
Db 439 GTGGGTGTCACCGGAAACCGGATTTGAGAACAGTTTCCAGATGAAGCTACTGTATGGGCT 498  
Qy 481 TGTGGCAACCAAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540  
Db 499 TGTGGCAACCAAAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 558

QY 541 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACT 600  
DB 559 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACT 618  
QY 601 ATACTGCTGTGAGGAAATGCAATTAATCTTTGTTAGCAGGAGATTGCAACCTGCAT 660  
DB 619 ATACTGCTGTGAGGAAATGCAATTAATCTTTGTTAGCAGGAGATTGCAACCTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCCAAGCTTGTGCTTCCAGTAGATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCCAAGCTTGTGCTTCCAGTAGATCC 738  
QY 721 GGAATAATTCGAAAGAAAGAAATTTAAACATCTTAATATGTCATCTGTGCTTATG 780  
DB 739 GGAATAATTCGAAAGAAAGAAATTTAAACATCTTAATATGTCATCTGTGCTTATG 798  
QY 781 GCTTATTTGCTTTATGTTGTTATGTCAGAAATTAATATGACAGATGAGAAACAAATCA 840  
DB 799 GCTTATTTGCTTTATGTTGTTATGTCAGAAATTAATATGACAGATGAGAAACAAATCA 858  
QY 841 TTGCTGATTTATTCACCAAGTTTATTAATATACAGTCACTTTTCAAAAATTGATTT 900  
DB 859 TTGCTGATTTATTCACCAAGTTTATTAATATACAGTCACTTTTCAAAAATTGATTT 918  
QY 901 TTTATATATTAATCTAGCTGCTATTCAAATGAGTCAACATTTTAAATTTATGTTCAAC 960  
DB 919 TTTATATATTAATCTAGCTGCTATTCAAATGAGTCAACATTTTAAATTTATGTTCAAC 978  
QY 961 TGTGTTGAGACTGAT 977  
DB 979 TGTGTTGAGACTGAT 995

RESULT 13  
ADL83254  
ID ADL83254 standard; cDNA; 1142 BP.  
XX  
AC ADL83254;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human PRO35972 cDNA, SEQ ID 456.  
XX  
KM Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
KM Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
KM Gene Therapy; PRO; B cell related disorder; cancer;  
KM Immune-mediated inflammatory disease; human; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024097-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003WO-US029097.  
XX  
PR 16-SEP-2002; 2002US-0411392P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
PI Wu TD;  
XX  
DR WPI; 2004-329389/30.  
XX  
PT P-PDB; ADL83255.  
XX  
XX New PRO polypeptide, useful for diagnosing and treating a B cell related  
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
XX  
PS Claim 2; Fig 456; 695BP; English.  
XX  
CC The present invention relates to PRO proteins and their coding sequences.

CC The PRO proteins are useful for diagnosing and treating a B cell related  
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide  
CC antigen unresponsiveness, selective IgA deficiency, immunodeficiency with  
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with  
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic  
CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.  
XX  
SQ Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
Query Match 99.3%; Score 972.2; DB 12; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GGAAGCCTTGGCCAGCGGCGCCGACCCCTGACCAATGACCCTGCGCCCTGG 60  
DB 19 GGAAGCCTTGGCCAGCGGCGCCGACCCCTGACCAATGACCCTGCGCCCTGG 78  
QY 61 GGCTGTCAATTCGTCTCTTTCTGACGAGGCTGCACTGGGCGATGCTCTAGAGC 120  
DB 79 GGCTGTCAATTCGTCTCTTTCTGACGAGGCTGCACTGGGCGATGCTCTAGAGC 138  
QY 121 CAACAGAAATTAAGCGGAGATCTGTCTCTGCCCCCTGACATGAGCACTCGCGGCCC 180  
DB 139 CAACAGAAATTAAGCGGAGATCTGTCTCTGCCCCCTGACATGAGCACTCGCGGCCC 198  
QY 181 TACTTCTCGTTACTACTACAGATCAAGTCAAGAGTCCGCAATTCCTGACGAGG 240  
DB 199 TACTTCTCGTTACTACTACAGATCAAGTCAAGAGTCCGCAATTCCTGACGAGG 258  
QY 241 GCTGCGAGGCAAGCCCAATTTCTACACTGGAGGCTTGGCAAGATGCTTCTGGA 300  
DB 259 GCTGCGAGGCAAGCCCAATTTCTACACTGGAGGCTTGGCAAGATGCTTCTGGA 318  
QY 301 GGATAGAAAAGTTCCCAAGTTTCCGAGTGAAGTGAAGCAAGTGTGAGG 360  
DB 319 GGATAGAAAAGTTCCCAAGTTTCCGAGTGAAGTGAAGCAAGTGTGAGG 378  
QY 361 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAATTTCTTTCCG 420  
DB 379 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTGAAAATTTCTTTCCG 438  
QY 421 GTGGGTGACCCGAAACCGAATTGAAACAGTTTCCAGTGAAGTACTTGTATGGGCT 480  
DB 439 GTGGGTGACCCGAAACCGAATTGAAACAGTTTCCAGTGAAGTACTTGTATGGGCT 498  
QY 481 TCTGCGACCAAGAAATTCATCATTTTGTACAGTCCAAAGTAAGTGAAGGAGTGTCT 540  
DB 499 TCTGCGACCAAGAAATTCATCATTTTGTACAGTCCAAAGTAAGTGAAGGAGTGTCT 558  
QY 541 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACT 600  
DB 559 CTGCAATGTGACCTGCTATTATTTAAATCCAAAGATACAGACCTGTATGCTTCACT 618  
QY 601 ATACTGCTGTGAGGAAATGCAATTAATCTTTGTTAGCAGGAGATTGCAACCTGCAT 660  
DB 619 ATACTGCTGTGAGGAAATGCAATTAATCTTTGTTAGCAGGAGATTGCAACCTGCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCCAAGCTTGTGCTTCCAGTAGATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATCCCAAGCTTGTGCTTCCAGTAGATCC 738  
QY 721 GGAATAATTCGAAAGAAAGAAATTTAAACATCTTAATATGTCATCTGTGCTTATG 780  
DB 739 GGAATAATTCGAAAGAAAGAAATTTAAACATCTTAATATGTCATCTGTGCTTATG 798

QY 761 GCTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
DB 769 GCTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGGGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
DB 859 TTGGGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 918  
QY 901 TTTATATATTAACCTGCTATTCACAAATGAGTCACTATTTTAAATTTATGTTCAAC 960  
DB 919 TTTATATATTAACCTGCTATTCACAAATGAGTCACTATTTTAAATTTATGTTCAAC 978  
QY 961 TGTTTGTGAGCTGAAT 977  
DB 979 TGTTTGTGAGCAAAAT 995

RESULT 14  
ADU06173  
ID ADU06173 standard; DNA; 1142 BP.  
AC ADU06173;  
XX 27-JAN-2005 (first entry)  
DT  
XX Novel bronchial cancer-associated human gene SeqIDJ397.  
XX  
XX bronchial cancer; cytostatic; tumour-associated protein;  
XX cancer detection; metastasis; tumour; gene; ds; human.  
XX Homo sapiens.  
XX  
XX DE10316701-A1.  
XX  
XX 04-NOV-2004.  
XX  
XX 09-APR-2003; 2003DE-01016701.  
XX  
XX 09-APR-2003; 2003DE-01016701.  
XX  
XX 09-APR-2003; 2003DE-01016701.  
XX  
XX (HINZ/) HINZMANN B.  
XX (HERM/) HERMANN K.  
XX (CAST/) HEIDEN CASTANOS-VELEZ E.  
XX  
XX Mennerich D, Bruemendorf T, Heiden B, Hermann K, Kinnemann H;  
XX Li X, Roepcke S, Staub B, Hinzmann B, Rosenthal A, Pilarsky C;  
XX WPI; 2004-786403/78.  
XX P-PSDB; ADU06660.  
XX  
XX New nucleic acid, and derived proteins, useful for diagnosis of bronchial  
XX cancer and in screening for therapeutic and diagnostic agents.  
XX  
XX Claim 1; SEQ ID NO 397; 1381bp; German.

This invention relates to a novel isolated nucleic acid associated with  
bronchial cancer comprising 489 defined sequences given in the  
specification. The invention may be useful for the production of  
compounds with a cytostatic activity through the inhibition of expression  
or activity of tumour-associated proteins. The novel DNA sequences and  
the proteins/peptides encoded by them are used for detecting bronchial  
cancer or determining the risk of developing it and to screen for  
specific binding partners of the DNA or protein sequences, where the  
binding partners are potentially useful as agents for treating or  
diagnosing bronchial cancer. The DNA or protein sequences can also be  
used for prognosis, detection of metastases and for secondary treatment  
(of tumours that have been stabilised or are no longer detectable).  
Detecting abnormal expression of the DNA sequences provides early  
diagnosis of bronchial cancers. The present sequence is that of a novel  
bronchial cancer-associated human gene sequence of the invention.

Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;

Query Match 99.3%; Score 972.2; DB 13; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAGGCTTCGCCAGCGGGCGCGCCGACCCCTTGACATGAGCCCGCTGCGCCCTG 60  
DB 19 GGAGCGCCCTTGCGCCAGCGGGCGCGCCGACCCCTTGACATGAGCCCGCTGCG 78  
QY 61 GGCGTGTGATCTGCTGCTTTTCCGACGAGGGCTGCACTGGGAGAGCTGCTGAGAGC 120  
DB 79 GGCGTGTGATCTGCTGCTTTTCCGACGAGGGCTGCACTGGGAGAGCTGCTGAGAGC 138  
QY 121 CAACAGAAATTAACGCGAGATCTGCTCTCGCCCTAGACTACGGAACCTGCGCGGCC 180  
DB 139 CAACAGAAATTAACGCGAGATCTGCTCTCGCCCTAGACTACGGAACCTGCGCGGCC 198  
QY 181 TACTTCTCCGTTACTACTACAGAGTACAGCGACGAGGCTGCGCGCCGCTGTAAGG 240  
DB 199 TACTTCTCCGTTACTACTACAGAGTACAGCGACGAGGCTGCGCGCCGCTGTAAGG 258  
QY 241 GCTGAGAGGGCAAGCGCAATTTCTACACTGGAGGCTTGGCGAGAGCTTGGCTG 300  
DB 259 GCTGAGAGGGCAAGCGCAATTTCTACACTGGAGGCTTGGCGAGAGCTTGGCTG 318  
QY 301 GGATAGAAAAAGTTCCCAAGTTTGCAGGCTGCAAGTGAAGTGAAGCAAGTGAAG 360  
DB 319 GGATAGAAAAAGTTCCCAAGTTTGCAGGCTGCAAGTGAAGTGAAGCAAGTGAAG 378  
QY 361 GGTCCACAGAAAGATTTCTTTATATCTTAATGTTCAATGACATGTAAGAAATTTCTTCCG 420  
DB 379 GGTCCACAGAAAGATTTCTTTATATCTTAATGTTCAATGACATGTAAGAAATTTCTTCCG 438  
QY 421 GTGGGATGCAACGGAAACGGATGAGAACAGTTTCCAGATGAAGCTTGTATGGGCT 480  
DB 439 GTGGGATGCAACGGAAACGGATGAGAACAGTTTCCAGATGAAGCTTGTATGGGCT 498  
QY 481 TCTGCGCACCAAGAAAAATTCATATTTTGTCTACAGTCCAAAGAGTGAAGGAGCT 540  
DB 499 TCTGCGCACCAAGAAAAATTCATATTTTGTCTACAGTCCAAAGAGTGAAGGAGCT 558  
QY 541 CTGCGCAATGTGACCTCGCTATTTTATTAATCCAGATACAGAACTGTGATGCTTCACT 600  
DB 559 CTGCGCAATGTGACCTCGCTATTTTATTAATCCAGATACAGAACTGTGATGCTTCACT 618  
QY 601 ATACTGCTGTGAGGAGATGACATTAATCTTTAGAGAGGAGATTTGCAAGGTGAT 660  
DB 619 ATACTGCTGTGAGGAGATGACATTAATCTTTAGAGAGGAGATTTGCAAGGTGAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGCCTTGCCAGTGAATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGCCTTGCCAGTGAATCC 738  
QY 721 GGAATAATTCGAGAGAGCAATTTTAAACATTTCTTAATATGATCTGTTGTCTTATG 780  
DB 739 GGAATAATTCGAGAGAGCAATTTTAAACATTTCTTAATATGATCTGTTGTCTTATG 798  
QY 781 GCTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
DB 799 GCTATTTGCTTTATGTTGATCTGAAGATTAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGGGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
DB 859 TTGGGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 918  
QY 901 TTTATATATTAACCTGCTATTCACAAATGAGTCACTATTTTAAATTTATGTTCAAC 960  
DB 919 TTTATATATTAACCTGCTATTCACAAATGAGTCACTATTTTAAATTTATGTTCAAC 978  
QY 961 TGTTTGTGAGCTGAAT 977  
DB 979 TGTTTGTGAGCAAAAT 995



RESULT 15  
AD287319  
ID AD287319 standard; DNA; 1142 BP.  
AC AD287319;  
XX  
XX 28-JUN-2005 (first entry)  
DE Human tissue factor pathway inhibitor 2 (TFPI-2) DNA, SEQ ID NO: 23.  
XX  
XX Selectable marker; metabolic disorder; metabolic; screening;  
KM tissue factor pathway inhibitor 2; gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH 57..764  
FT CDS /tag= a  
FT /product= "Human tissue factor pathway inhibitor 2  
FT protein"  
XX  
XX EPI533619-A2.  
XX  
XX 25-MAY-2005.  
XX  
XX 12-NOV-2004; 2004EP-00026956.  
XX  
XX 20-NOV-2003; 2003US-0523845P.  
XX  
XX (HOF ) HOFMANN LA ROCHÉ & CO AG F.  
XX  
XX Kochan JP, Rosnaki JA,  
XX  
XX WPI; 2005-368646/38.  
XX  
XX P-Psdb; AD287320.  
XX  
XX DDBJ; D29992.  
XX  
XX REFSEQ; NM\_006528.  
XX  
XX Use of nucleic acids having nucleotide bases with specific nucleic acid  
XX PT sequences, and polypeptides with specific amino acid sequences as markers  
XX in the diagnosis of visceral adipose tissue accumulation.  
XX  
XX Claim 7; SEQ ID NO 23; 139bp; English.  
XX  
XX The present invention relates to a method for measurement of levels of  
XX CC visceral adipose tissue using markers. The invention also provides  
XX CC visceral adipose secreted proteins and their nucleic acids which are used  
XX CC as markers. The invention is useful in screening assays for identifying a  
XX CC compound that interacts with the visceral adipose secreted proteins and  
XX CC in the treatment of metabolic syndrome. The present sequence is human  
XX CC tissue factor pathway inhibitor 2 (TFPI-2; also termed as PPS, placental  
XX CC protein 5) coding DNA sequence which encodes one such adipose secreted  
XX CC protein.  
XX  
XX Sequence 1142 BP; 316 A; 248 C; 260 G; 318 T; 0 U; 0 Other;  
SQ

Query Match 99.3%; Score 972.2; DB 14; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 9.9e-256;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAAGCGCTTGGCCGAGGCGGCGCCGAGCCCTCTGACCATGACCCCGCTGCGCCCTTGG 60  
DB 19 GAGCGCGCTTGGCCGAGGCGGCGCCGAGCCCTCTGACCATGACCCCGCTGCGCCCTTGG 78  
QY 61 GAGCTGCGATTTGCTGCTTTTCTGACGAGGAGCTGCACTGAGGCGATGCTGCTCAGAGAC 120  
DB 79 GAGCTGCGATTTGCTGCTTTTCTGACGAGGAGCTGCACTGAGGCGATGCTGCTCAGAGAC 138  
QY 121 CAACAGGAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGGAACCTGCGCGGCGCC 180  
DB 139 CAACAGGAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGGAACCTGCGCGGCGCC 198

QY 181 TACTTCTCCGTTACTACTACGACAGTACACGACAGAGCTGCCGCACTTCTGTACGGGG 240  
DB 199 TACTTCTCCGTTACTACTACGACAGTACACGACAGAGCTGCCGCACTTCTGTACGGGG 258  
QY 241 GCTGCGAGGCGACCGCAACATTTCTACACTTGGAGGCTTGGGACGATGCTTGTGGA 300  
DB 259 GCTGCGAGGCGACCGCAACATTTCTACACTTGGAGGCTTGGGACGATGCTTGTGGA 318  
QY 301 GGATGAAAAAGTTCCCAAGTTTGGCGGCTGCAAGTGAAGTGGACGACGATGTGAGG 360  
DB 319 GGATGAAAAAGTTCCCAAGTTTGGCGGCTGCAAGTGAAGTGGACGACGATGTGAGG 378  
QY 361 GATCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGTAAATTTCTTTCG 420  
DB 379 GATCCACAGAAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGTAAATTTCTTTCG 438  
QY 421 GTGGGTGTCACCGAACCAGATTGAGAACAGGTTCCAGTGAAGTCTATGAGGCT 480  
DB 439 GTGGGTGTCACCGAACCAGATTGAGAACAGGTTCCAGTGAAGTCTATGAGGCT 498  
QY 481 TCTGGGACCAAAAAGTATTTCTATGATTTGCTACAGTCCAAAAGTGAAGGAGCTGAGT 540  
DB 499 TCTGGGACCAAAAAGTATTTCTATGATTTGCTACAGTCCAAAAGTGAAGGAGCTGAGT 558  
QY 541 CTGCCAATGTGACTCGCTATTATTATTTAATCCAGATACAGAACTGTGATGCTTCACT 600  
DB 559 CTGCCAATGTGACTCGCTATTATTATTTAATCCAGATACAGAACTGTGATGCTTCACT 618  
QY 601 ATACTGGCTGTGAGGAGGAAATGCAATTAATTTGTTAGGAGGAGATTGCAACGTCAT 660  
DB 619 ATACTGGCTGTGAGGAGGAAATGCAATTAATTTGTTAGGAGGAGATTGCAACGTCAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTGGCTGCGATGATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAAGAAAGATGCCAAAGCTTGGCTGCGATGATCC 738  
QY 721 GGAATATTCGAAAGAGCAATTTTAACATTTCTTAATATGTCATCTTGTGCTTTATG 780  
DB 739 GGAATATTCGAAAGAGCAATTTTAACATTTCTTAATATGTCATCTTGTGCTTTATG 798  
QY 781 GCTTATTTGCTTTATGCTTGTGATCTGAAGATATATGACAGCATGAGGAAACAAATCA 840  
DB 799 GCTTATTTGCTTTATGCTTGTGATCTGAAGATATATGACAGCATGAGGAAACAAATCA 858  
QY 841 TTGGTGAATTTATTCACAGTTTATTAATTAACAAGTCACTTTCAAAAATTTGATTTT 900  
DB 859 TTGGTGAATTTATTCACAGTTTATTAATTAACAAGTCACTTTTCAAAAATTTGATTTT 918  
QY 901 TTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960  
DB 919 TTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 978  
QY 961 TGTGTTGAGACTGAAT 977  
DB 979 TGTGTTGAGACTGAAT 995

Search completed: March 11, 2006, 07:11:44  
Job time : 637 secs



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Best Local Similarity 99.9%; Pred. No. 7.8e-244; Matches 978; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGACGCGCTTGCCGAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTG 60
Db 21 GGACGCGCTTGCCGAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTG 80
OY 61 GCGCTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGAGTGTCTGACAGAGC 120
Db 81 GCGCTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGAGTGTCTGACAGAGC 140
OY 121 CAACGGAATAACGGGAGATCTGTCTGCTGCTTACATACGAGACCTGCGCGGCGCC 180
Db 141 CAACGGAATAACGGGAGATCTGTCTGCTGCTTACATACGAGACCTGCGCGGCGCC 200
OY 181 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGAGTTCTGTACGGGG 240
Db 201 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGAGTTCTGTACGGGG 260
OY 241 GCTGCGAGGGCAACGCGCAATTTCTACACCTGGAGGCTTGCGAGATGCTGTCTGGA 300
Db 261 GCTGCGAGGGCAACGCGCAATTTCTACACCTGGAGGCTTGCGAGATGCTGTCTGGA 320
OY 301 GGATGAAAAAGTTTCCCAAGTTTGGCGGCTGCAATGTGTGACACACATGTGAGG 360
Db 321 GGATGAAAAAGTTTCCCAAGTTTGGCGGCTGCAATGTGTGACACACATGTGAGG 380
OY 361 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCCATGACATGTGAAAAATCTTTTCCG 420
Db 381 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCCATGACATGTGAAAAATCTTTTCCG 440
OY 421 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAGTACTGTATGGGCT 480
Db 441 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAGTACTGTATGGGCT 500
OY 481 TGTGGGCAACAAAGAAATTTCCATGCTTTTGTCTACAGTCCAAAAGATGAGGACCTGTGT 540
Db 501 TGTGGGCAACAAAGAAATTTCCATGCTTTTGTCTACAGTCCAAAAGATGAGGACCTGTGT 560
OY 541 CTGCCAATGTGACTCGCTATTTATTTAATCCAAGATACAGAACTGTGATGCTTCACT 600
Db 561 CTGCCAATGTGACTCGCTATTTATTTAATCCAAGATACAGAACTGTGATGCTTCACT 620
OY 601 AATCTGCTGTGAGGGAATGACAATTAATTTGTTAGCAGGAGATTCGCAACGTCAT 660
Db 621 AATCTGCTGTGAGGGAATGACAATTAATTTGTTAGCAGGAGATTCGCAACGTCAT 680
OY 661 GTGCAAAAGCTTTGAAAAAGAAAGATATGCCAAAGCTTGGCTTGGCAATGAAATCC 720
Db 681 GTGCAAAAGCTTTGAAAAAGAAAGATATGCCAAAGCTTGGCTTGGCAATGAAATCC 740
OY 721 GGAATAATTCGAAAGAACATTTTAAACATTTTAATATGTCACTTGTGTTGCTTATG 780
Db 741 GGAATAATTCGAAAGAACATTTTAAACATTTTAATATGTCACTTGTGTTGCTTATG 800
OY 781 GCTTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAAACAATCA 840
Db 801 GCTTATTTGCTTTATGTTGTATCTGAAGAAATATATGACAGATGAGAAAACAATCA 860
OY 841 TTGGTGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTTT 900
Db 861 TTGGTGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTTGGATTTT 920
OY 901 TTTATATATATACAGTGTCTATTCAAATGTGAGTCAATTTTAAATTTATGTTTCAAC 960
Db 921 TTTATATATATACAGTGTCTATTCAAATGTGAGTCAATTTTAAATTTATGTTTCAAC 980
OY 961 TGTTTGTGAGACTGAATTC 979
Db 981 TGTTTGTGAGACTGAATTC 999

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RESULT 2

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CR601552
LOCUS CR601552 1002 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1036YK11 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR601552
VERSION CR601552.1 GI:50482359
KEYWORDS HTC; CNSLT; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1002)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization.
Unpublished
Contact: Feng Liang Email: fliang@lifestech.com URL:
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Paradise Avenue
2 (bases 1 to 1002)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:
BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source 1..1002
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1036YK11"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 99.8%; Score 977.4; DB 4; Length 1002;
Best Local Similarity 99.9%; Pred. No. 1.6e-243;
Matches 978; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 GGACGCGCTTGCCGAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTG 60
Db 3 GGACGCGCTTGCCGAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTG 62
OY 61 GCGCTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGAGTGTCTGACAGAGC 120
Db 63 GCGCTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGAGTGTCTGACAGAGC 122
OY 121 CAACGGAATAACGGGAGATCTGTCTGCTTACATACGAGACCTGCGCGGCGCC 180
Db 123 CAACGGAATAACGGGAGATCTGTCTGCTTACATACGAGACCTGCGCGGCGCC 182
OY 181 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGAGTTCTGTACGGGG 240
Db 183 TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCGAGTTCTGTACGGGG 242
OY 241 GCTGCGAGGGCAACGCGCAATTTCTACACCTGGAGGCTTGCGAGATGCTGTCTGGA 300
Db 243 GCTGCGAGGGCAACGCGCAATTTCTACACCTGGAGGCTTGCGAGATGCTGTCTGGA 302
OY 301 GGATGAAAAAGTTTCCCAAGTTTGGCGGCTGCAATGTGTGACACACATGTGAGG 360
Db 303 GGATGAAAAAGTTTCCCAAGTTTGGCGGCTGCAATGTGTGACACACATGTGAGG 362
OY 361 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCCATGACATGTGAAAAATCTTTTCCG 420
Db 363 GGTCCACAGAAAAGTATTTCTTAACTTAAGTTCCATGACATGTGAAAAATCTTTTCCG 422
OY 421 GTGGGTGTCAACCGGAACCGGATTTAGAACAGGTTTCCAGATGAAGTACTGTATGGGCT 480

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Db      423 GTGGGTGTCAACGGAAACCGGATTTGAGACAGGTTTCAGATGAGTACTGTTATGAGGCT 482
Qy      481 TCTGGGACCAAAAGAAATTCATCATCTTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540
Db      483 TCTGGGACCAAAAGAAATTCATCATCTTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 542
Qy      541 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGGAGCTGTGATGCTTTCACCT 600
Db      543 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGGAGCTGTGATGCTTTCACCT 602
Qy      601 ATACTGCTGTGAGGAGGATGACAATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT 660
Db      603 ATACTGCTGTGAGGAGGATGACAATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT 662
Qy      661 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTTCGCTTTCAGTAGAATCC 720
Db      663 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTTCGCTTTCAGTAGAATCC 722
Qy      721 GGAATAATTCGGAAGAGCAATTTTAAACATCTCTTAATATGTCATCTGTGTTGCTTTATG 780
Db      723 GGAATAATTCGGAAGAGCAATTTTAAACATCTCTTAATATGTCATCTGTGTTGCTTTATG 782
Qy      781 GCTTATTTGCTTTTATGTTTATCTGATCTGAGAAATTAATATGACAGATGAGAAACAATCA 840
Db      783 GCTTATTTGCTTTTATGTTTATCTGATCTGAGAAATTAATATGACAGATGAGAAACAATCA 842
Qy      841 TTGGTATTTATTCACACGATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 900
Db      843 TTGGTATTTATTCACACGATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 902
Qy      901 TTTATATATTAATAGCTGCTATTTCAAAATGTGAGTCAACATTTTAAATTATGTTCAAC 960
Db      903 TTTATATATTAATAGCTGCTATTTCAAAATGTGAGTCAACATTTTAAATTATGTTCAAC 962
Qy      961 TGTGTGTGAGCTGAATTC 979
Db      963 TGTGTGTGAGCTGAATTC 981

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RESULT 3
CR605727      1006 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS      full-length cDNA clone CS0D1042Yp21 of Placenta Cot 25-normalized
DEFINITION
ACCESSION      CR605727
VERSION      CR605727.1 GI:50486534
KEYWORDS      HTC; CNSLT cDNA.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1006)
L1.W.B., Gruber, C., Jessee, J. and Polyes, D.
Unpublished
Full-length cDNA libraries and normalization
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1006)
Genoscope.
Direct Submision
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.
FEATURES
source      1..1006
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1042Yp21"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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ORIGIN
Query Match      99.8%; Score 977.4; DB 4; Length 1006;
Best Local Similarity 99.8%; Pred.No.1:6e-243;
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAAGCCCTTGGCCCAAGCGGCGCCCGACCCCTGTGACCAATGACCCCGCTCGCCCTG 60
Db      26  GGAAGCCCTTGGCCCAAGCGGCGCCCGACCCCTGTGACCAATGACCCCGCTCGCCCTG 85
Qy      61  GGCTGTGATTCGTGCTCTTTTCTGTACGAGAGGCTGCACTGGGCAATGCTGCTCAGAGC 120
Db      86  GGCTGTGATTCGTGCTCTTTTCTGTACGAGAGGCTGCACTGGGCAATGCTGCTCAGAGC 145
Qy      121 CAACAGAAATPACCGGAGATCTGTCTCCCTGACCTAGCTACGGAACCTGCGCGGCGCC 180
Db      146 CAACAGAAATPACCGGAGATCTGTCTCCCTGACCTAGCTACGGAACCTGCGCGGCGCC 205
Qy      181 TACTTCTCCGTTACTACTACAGAGTACACGAGAGTCCCGCAGTTCTGTACGAGG 240
Db      206 TACTTCTCCGTTACTACTACAGAGTACACGAGAGTCCCGCAGTTCTGTACGAGG 265
Qy      241 GCTGCGAGGCGCAAGCGCAATTTCTACACTGTGAGGCTTTCGACGATGCTTGCTGCA 300
Db      266 GCTGCGAGGCGCAAGCGCAATTTCTACACTGTGAGGCTTTCGACGATGCTTGCTGCA 325
Qy      301 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGAGACGACGAGTGTGAGG 360
Db      326 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGAGACGACGAGTGTGAGG 385
Qy      361 GGTCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGATGATGAAAAATCTTTCCG 420
Db      386 GGTCACAGAAAAAGTATTTCTTAAATCTAAGTTCATGATGATGAAAAATCTTTCCG 445
Qy      421 GTGGGTGTCAACGGAAACCGGATTTGAGAACAGGTTTCCAGATGAGCTACTGTATGAGGCT 480
Db      446 GTGGGTGTCAACGGAAACCGGATTTGAGAACAGGTTTCCAGATGAGCTACTGTATGAGGCT 505
Qy      481 TCTGGGACCAAAAGAAATTCATCATCTTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540
Db      506 TCTGGGACCAAAAGAAATTCATCATCTTTTGTCTACAGTCCAAAAGATGAGGAGCTGTGCT 565
Qy      541 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGGAGCTGTGATGCTTTCACCT 600
Db      566 CTGCCAATGTGACTGCTATTTATTTAATCCAAAGATGAGGAGCTGTGATGCTTTCACCT 625
Qy      601 ATACTGCTGTGAGGAGGATGACAATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT 660
Db      626 ATACTGCTGTGAGGAGGATGACAATTAATCTTTGTAGCAGGAGATTCGCAACGTGCAT 685
Qy      661 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTTCGCTTTCAGTAGAATCC 720
Db      686 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTTCGCTTTCAGTAGAATCC 745
Qy      721 GGAATAATTCGGAAGAGCAATTTTAAACATCTCTTAATATGTCATCTGTGTTGCTTTATG 780
Db      746 GGAATAATTCGGAAGAGCAATTTTAAACATCTCTTAATATGTCATCTGTGTTGCTTTATG 805
Qy      781 GCTTATTTGCTTTTATGTTTATCTGATCTGAGAAATTAATATGACAGATGAGAAACAATCA 840
Db      806 GCTTATTTGCTTTTATGTTTATCTGAGAAATTAATATGACAGATGAGAAACAATCA 865
Qy      841 TTGGTATTTATTAATAGCTGCTATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 900
Db      866 TTGGTATTTATTAATAGCTGCTATTTTATTAATACAGTCACTTTTTCAAAAATTTGATTTT 925
Qy      901 TTTATATATTAATAGCTGCTATTTCAAAATGTGAGTCAACATTTTAAATTATGTTCAAC 960

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Db      926 TTTAATATTAAGTCTGATTCATTCATTAATGATGATCTACCAATTTTAAATTATGTTCAAC 985
Qy      961 TGTGTGTGAGACTGAATTC 979
Db      986 TGTGTGTGAGACTGAATTC 1004

RESULT 4
CR615838
LOCUS    full-length cDNA clone CS0D1075YF03 of Placenta Cot 25-normalized
DEFINITION
ACCESSION CR615838
VERSION   CR615838.1 GI:50496645
KEYWORDS  HTC; CNSLT CDNA.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
          1 (bases 1 to 1007)
          Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1007)
          Genoscope.
          Direct Submission
          Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
          Location/Qualifiers
            source          1..1007
                           /organism="Homo sapiens"
                           /mol_type="mRNA"
                           /db_xref="taxon:9606"
                           /clone="CS0D1075YF03"
                           /issue_type="Placenta Cot 25-normalized"
                           /plasmid="pCMVSPORT_6"

ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1007;
Best Local Similarity 99.9%; Pred. No. 1,6e-243;
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGAGGCGCTTGGCCAGGCGGCGCCGACCCCTGTGACCAATGACCCCGCTGCGCCCGCG 60
Db      3  GGAGGCGCTTGGCCAGGCGGCGCCGACCCCTGTGACCAATGACCCCGCTGCGCCCGCG 62
Qy      61  GGCTGTCAATTCGTGCTGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 120
Db      63  GGCTGTCAATTCGTGCTGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 122
Qy      121  CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTTGGCGGCGCC 180
Db      123  CAACGAGAAATACGCGGAGATCTGCTCTGCGCCCTAGACTACGAGACCTTGGCGGCGCC 182
Qy      181  TACTTCTCCGTTACTACTACGACAGGTACAGGAGCTGCGCGCAAGTTCCTGTACGGGG 240
Db      183  TACTTCTCCGTTACTACTACGACAGGTACAGGAGCTGCGCGCAAGTTCCTGTACGGGG 242
Qy      241  GCTGGAGGGGCAACGCCAATTTCTACACTGTGGAGGCTTGGCAGACATGCTTCTGGA 300
Db      243  GCTGGAGGGGCAACGCCAATTTCTACACTGTGGAGGCTTGGCAGACATGCTTCTGGA 302

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Qy      301  GGATAGAAAAAGTCTCCAAAGTTTGCOCGCTGCAAGTGAATGTGACGACAGTGTGAG 360
Db      303  GGATAGAAAAAGTCTCCAAAGTTTGCOCGCTGCAAGTGAATGTGACGACAGTGTGAG 362
Qy      361  GGTCCACGAAAAAGTATTTCTTAACTTAAGTTCATGATCATGTGAAAAATTTCTTCCG 420
Db      363  GGTCCACGAAAAAGTATTTCTTAACTTAAGTTCATGATCATGTGAAAAATTTCTTCCG 422
Qy      421  GTGGGTGTCAACCGGAGACGGATTTGAGAAACAGGTTTCCAGATAGACTACTTATGGGCT 480
Db      423  GTGGGTGTCAACCGGAGACGGATTTGAGAAACAGGTTTCCAGATAGACTACTTATGGGCT 482
Qy      481  TCTGCGCACCAAGAAAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540
Db      483  TCTGCGCACCAAGAAAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 542
Qy      541  CTGCGCAATGTGACTCTGCTATTTTAACTTCAAGATACAGAACTGTGATGCTTTCACT 600
Db      543  CTGCGCAATGTGACTCTGCTATTTTAACTTCAAGATACAGAACTGTGATGCTTTCACT 602
Qy      601  AATCTGCTGTGAGAGGAATGACATTAATCTTTAGAGGAGGAGATTGCAGAACGTGAT 660
Db      603  AATCTGCTGTGAGAGGAATGACATTAATCTTTAGAGGAGGAGATTGCAGAACGTGAT 662
Qy      661  GTGCAAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGTGCTTGCAGTAGAATCC 720
Db      663  GTGCAAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAAGCTTGTGCTTGCAGTAGAATCC 722
Qy      721  GGAATAATTCGAGAGAGCAATTTTAAATCTTAAATATGTCATCTTGTGCTTTATG 780
Db      723  GGAATAATTCGAGAGAGCAATTTTAAATCTTAAATATGTCATCTTGTGCTTTATG 782
Qy      781  GCTTATTTGCTTTATGTTGATCTGATCTGAAGATATATAGACAGATGAGAGAAACAATCA 840
Db      783  GCTTATTTGCTTTATGTTGATCTGATCTGAAGATATATAGACAGATGAGAGAAACAATCA 842
Qy      841  TTGGTATTTATTCACCAAGTTTATTAATTAACAAGTCACTTTTCMAAAATTTGGAATTT 900
Db      843  TTGGTATTTATTCACCAAGTTTATTAATTAACAAGTCACTTTTCMAAAATTTGGAATTT 902
Qy      901  TTTAATATTAATCTAGCTGCTATTCGAAATGTGAGTCTACATTTTAAATTATGTTCAAC 960
Db      903  TTTAATATTAATCTAGCTGCTATTCGAAATGTGAGTCTACATTTTAAATTATGTTCAAC 962
Qy      961  TGTGTGTGAGACTGAATTC 979
Db      963  TGTGTGTGAGACTGAATTC 981

RESULT 5
CR620705
LOCUS    full-length cDNA clone CS0D1064YJ18 of Placenta Cot 25-normalized
DEFINITION
ACCESSION CR620705
VERSION   CR620705.1 GI:50501512
KEYWORDS  HTC; CNSLT CDNA.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
          1 (bases 1 to 1009)
          Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1009)
          Genoscope.
          Direct Submission
          Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

```

## COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

## FEATURES

Location/Qualifiers  
1..1009

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS001031YL22"  
/issue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1009;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAGCGCTTGGCCGAGGCGGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
20 GGACGCGCTTGGCCGAGGCGGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 79  
61 GGCTGTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 120  
80 GGCTGTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 139  
121 CAACGAGAAATACGCGGAGATCTGCTGCGCCCTGACATACGAGACCCCTGCGGCGCC 180  
140 CAACGAGAAATACGCGGAGATCTGCTGCGCCCTGACATACGAGACCCCTGCGGCGCC 199  
181 TACTTCTCCGTTACTACGACAGGTACACGAGAGTCCGCGCAGTTCTGTACGAGG 240  
200 TACTTCTCCGTTACTACGACAGGTACACGAGAGTCCGCGCAGTTCTGTACGAGG 259  
241 GCTGCGAGGCGCAACGCAATTTTACACCTGGAGGCTTGCACATGCTGCTGCA 300  
260 GCTGCGAGGCGCAACGCAATTTTACACCTGGAGGCTTGCACATGCTGCTGCA 319  
301 GGATGAGAAAGTTCCCAAGTTTGCAGGCTGCAATGAGTGAAGGCAAGTGAAG 360  
320 GGATGAGAAAGTTCCCAAGTTTGCAGGCTGCAATGAGTGAAGGCAAGTGAAG 379  
361 GGTCCACAGAAAGTATTTCTTAATCTAAGTCAATGATGTAAGAAATCTTTCCG 420  
380 GGTCCACAGAAAGTATTTCTTAATCTAAGTCAATGATGTAAGAAATCTTTCCG 439  
421 GTGGGTGTACCGGAAACCGGATTTGAGAACGTTTCAATGAACTTGTATGGGCT 480  
440 GTGGGTGTACCGGAAACCGGATTTGAGAACGTTTCAATGAACTTGTATGGGCT 499  
481 TCGGCGCACAAAGAAATTCATCTTGTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
500 TCGGCGCACAAAGAAATTCATCTTGTGCTACAGTCCAAAGATGAGGAGCTGTGCT 559  
541 CTGCGAATGTGACTCGCTATTTTATCTCAAGATACGAACCTGTGATGCTTTGACCT 600  
560 CTGCGAATGTGACTCGCTATTTTATCTCAAGATACGAACCTGTGATGCTTTGACCT 619  
601 ATACTGGCTGTGAGGGAATGACATTAATCTTTTACAGGAGGATTTGCAACGTCAT 660  
620 ATACTGGCTGTGAGGGAATGACATTAATCTTTTACAGGAGGATTTGCAACGTCAT 679  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGTGCAAGATGCT 720  
680 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGTGCAAGATGCT 739  
721 GGAATAATGGAAGAAATTTTAAACATCTTAAATATGTCATCTTGTGCTTAAAG 780  
740 GGAATAATGGAAGAAATTTTAAACATCTTAAATATGTCATCTTGTGCTTAAAG 799

QY 781 GCTATTTGCTTTATGTTGATCTGAGATATATATATGACAGATGAGAAACAATCA 840  
DB 800 GCTATTTGCTTTATGTTGATCTGAGATATATATATGACAGATGAGAAACAATCA 859  
QY 841 TTGGTATTTATTCACAGATTTTATATATACAGTCACTTTTCAAAAATTGATTT 900  
DB 860 TTGGTATTTATTCACAGATTTTATATATACAGTCACTTTTCAAAAATTGATTT 919  
QY 901 TTTATATATATACAGTCTATTCAAATGATGCTTACATTTTATATATATGTTCAAC 960  
DB 920 TTTATATATATACAGTCTATTCAAATGATGCTTACATTTTATATATATGTTCAAC 979  
QY 961 TGTGTTGAGACTGAATTC 979  
DB 980 TGTGTTGAGACTGAATTC 998

RESULT 6  
CR621703 1028 bp mRNA linear HTC 21-JUL-2004  
LOCUS  
DEFINITION  
full-length cDNA clone CS001031YL22 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
CR621703  
ACCESSION  
CR621703.1 GI:50502510  
VERSION  
HTC; CNSLT cDNA.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
1 (bases 1 to 1028)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Poyates, D.  
TITLES  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished  
REMARK  
Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Parade Avenue  
2 (bases 1 to 1028)

REFERENCE  
Genoscope.  
AUTHORS  
Direct Submision  
TITLES  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL  
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

## FEATURES

Location/Qualifiers  
1..1028

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS001031YL22"  
/issue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1028;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAGCGCTTGGCCGAGGCGGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
20 GGACGCGCTTGGCCGAGGCGGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 88  
61 GGCTGTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 120  
80 GGCTGTGCAATTCGCTGCTTTTCTGACGAGGCTGCACTGGGCGCATGCTGCTCAGAGAC 148  
121 CAACGAGAAATACGCGGAGATCTGCTGCGCCCTGACATACGAGACCCCTGCGGCGCC 180  
149 CAACGAGAAATACGCGGAGATCTGCTGCGCCCTGACATACGAGACCCCTGCGGCGCC 208

QY	181	TACTCTCCGTTACTACTCTACGAAAGGTACACGAGAGCTGCACGTCCTCTGTAAGGGG	240
Db	209	TACTCTCCGTTACTACTACAGAGGTACACGAGAGCTGCACGTCCTCTGTAAGGGG	268
QY	241	GCTGCGAGGGCAACCGCCAAACAATTTCTACACTGGAGGCTTGCGACGATGCTTGCTGGA	300
Db	269	GCTGCGAGGGCAACCGCCAAACAATTTCTACACTGGAGGCTTGCGACGATGCTTGCTGGA	328
QY	301	GGATGAAAAAGTTCCTCCAAAGTTTGCCGCTGCAATGAGTGTGAGACGACCAATGTGAGG	360
Db	329	GGATGAAAAAGTTCCTCCAAAGTTTGCCGCTGCAATGAGTGTGAGACGACCAATGTGAGG	398
QY	361	GGTCCACAGAAAAAGTATTTCTTTAATCTAAGTTCACATGACATGTAAGAAATCTTTCCG	420
Db	389	GGTCCACAGAAAAAGTATTTCTTTAATCTAAGTTCACATGACATGTAAGAAATCTTTCCG	448
QY	421	GTTGGGTGACCGGAACCGGATTTGAGACAGAGTTTCCAGATGAAGCTACTTGTATGAGGCT	480
Db	449	GTTGGGTGACCGGAACCGGATTTGAGACAGAGTTTCCAGATGAAGCTACTTGTATGAGGCT	508
QY	481	TCTGGGCAACCAAGAAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT	540
Db	509	TCTGGGCAACCAAGAAAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT	568
QY	541	CTGCCAATGTGACTGCGCTATTTATTTAATCCAAAGATACAGAACTGTGATGCTTCACT	600
Db	569	CTGCCAATGTGACTGCGCTATTTATTTAATCCAAAGATACAGAACTGTGATGCTTCACT	628
QY	601	ATACTGGCTGTGAGGGAATGACATAACTTTGTAGCGAGAGATTCGAAACGTGCAT	660
Db	629	ATACTGGCTGTGAGGGAATGACATAACTTTGTAGCGAGAGATTCGAAACGTGCAT	688
QY	661	GTCGCAAAAGCTTTGAAAAAGAAAAAGAGATGCGAAAGCTTGCTTGCGCAATGAATCC	720
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QY	721	GGAATAATTCGAGAGGCAATTTTAAACAATCTTAATATGTCATCTGTTGTCTTTATG	780
Db	749	GGAATAATTCGAGAGGCAATTTTAAACAATCTTAATATGTCATCTGTTGTCTTTATG	808
QY	781	GCTTATTTGCTTTATGTTGTGATCTGAGAAATTAATATGACGCAATGAGAAAACAATCA	840
Db	809	GCTTATTTGCTTTATGTTGTGATCTGAGAAATTAATATGACGCAATGAGAAAACAATCA	868
QY	841	TTGGATATTATTCACAGATTTTATTAATACAGTCACTTTTAAAAAATTTGGAATTT	900
Db	869	TTGGATATTATTCACAGATTTTATTAATACAGTCACTTTTAAAAAATTTGGAATTT	928
QY	901	TTTATATATACTAGCTGCTATTCGAATGTGAGTCTACACTTTTAAATTTATGTTCAAC	960
Db	929	TTTATATATACTAGCTGCTATTCGAATGTGAGTCTACACTTTTAAATTTATGTTCAAC	988
QY	961	TGTTTGAGACTGAATTC	979
Db	989	TGTTTGAGACTGAATTC	1007

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
CR615468	CR615468	1031 bp mRNA linear	CR615468	CR615468	HTC; cNSLT_cDNA.	Homo sapiens (human)	Homo sapiens	full-length cDNA clone CSD01068Y03 of Placenta Cot 25-normalized of Homo sapiens (human).	HTC 21-JUL-2004
					GI:50496275		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.		
							1 (bases 1 to 1031)		
								14, W. B., Gruber, C., Jeesee, J. and Polayes, D.	

TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Parade Avenue 2 (bases 1 to 1031) Genoscope. Direct Submission Submitted (20-UTL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1. 1031 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSOD1068YJ03" /issue_type="Placenta Cot 25-normalized" /plasmid="pCMVSPORT_6"
COMMENT	
FEATURES	
source	
ORIGIN	
Query Match	99.8%; Score 977.4; DB 4; Length 1031;
Best Local Similarity	99.9%; Pred. No. 1,66-243;
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
1	GGAGCGCTTGGCCGAGGGGCGGGCCGCGCCCTGACAGAGAGCCCGCTGCCCCCTGG 60
17	GGAGCGCTTGGCCGAGGGGCGGGCCGCGCCCTGACAGAGAGCCCGCTGCCCCCTGG 76
61	GGCTGTGATTTCTGCTCTTTTCTTCTGACGAGGCTGCACTGGCGATGCTTCTGAGAGC 120
77	GGCTGTGATTTCTGCTCTTTTCTTCTGACGAGGCTGCACTGGCGATGCTTCTGAGAGC 136
121	CAACAGAAATTAACGCGGAGATCTGTCTCTGCCCCCTAGCTAGAGACCTTGGCGGCC 180
137	CAACAGAAATTAACGCGGAGATCTGTCTCTGCCCCCTAGCTAGAGACCTTGGCGGCC 196
181	TACTTCTCGGTACTACTAGACAGGATACAGAGAGCTGGCCCGAGTTCTGTAGCGGG 240
197	TACTTCTCGGTACTACTAGACAGGATACAGAGAGCTGGCCCGAGTTCTGTAGCGGG 256
241	GCTGCGAGGGCAACGCGCAATTTCTTCACTCTGAGAGCTTGCAGATGCTTCTGAGAG 300
257	GCTGCGAGGGCAACGCGCAATTTCTTCACTCTGAGAGCTTGCAGATGCTTCTGAGAG 316
301	GGATAGAAAAGTTTCCCAAGTTTGGCCGGCTGCAAGTGAAGTGAAGCAACAGTGAAG 360
317	GGATAGAAAAGTTTCCCAAGTTTGGCCGGCTGCAAGTGAAGTGAAGCAACAGTGAAG 376
361	GGATAGAAAAGTTTCTTAATCTAAGTTCCATGACATGAGAAAATTTCTTTCCG 420
377	GGATAGAAAAGTTTCTTAATCTAAGTTCCATGACATGAGAAAATTTCTTTCCG 436
421	GTGGGTGTCAACCGGAACCGGATTTGAGAAACAGTTTCAATGAAAGCTATGATGGCT 480
437	GTGGGTGTCAACCGGAACCGGATTTGAGAAACAGTTTCAATGAAAGCTATGATGGCT 496
481	TTGGGCAACCAAGAAATTCATCTATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540
497	TTGGGCAACCAAGAAATTCATCTATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 556
541	CTGGCAATGTGACTGCTATTTATTTTAAATCCAAAGATGAGGAGCTGTCT 600
557	CTGGCAATGTGACTGCTATTTATTTTAAATCCAAAGATGAGGAGCTGTCT 616
601	ATATCTGGCTGTGAGGAGATGACATTAATTTTGTGAGGAGGAGATTTGCAACGTCAT 660
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QY 661 GTGCAAAAGCTTGAAGAGAGATGCAAGCTTGCTTGCCAGTAGAATCC 720  
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 QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATATGACAGCATGAGAAACAATCA 840  
 DB 797 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATATGACAGCATGAGAAACAATCA 856  
 QY 841 TTGGGATTTATTCACAGCTTTTATATATACAGCATCTTTTCAAAATTGATTT 900  
 DB 857 TTGGGATTTATTCACAGCTTTTATATATACAGCATCTTTTCAAAATTGATTT 916  
 QY 901 TTTATATATATACAGCTGCTATTCAAATGAGTCTACCATTTTATATATATGTTCAAC 960  
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 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 977 TGTTTGTGAGACTGAATTC 995  
 RESULT 8  
 CR612082 1033 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CSOD1012YJ24 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).  
 ACCESSION CR612082.1 GI:50492889  
 VERSION CR612082.1 GI:50492889  
 KEYWORDS HTC; CDS; cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 1033)  
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 1033)  
 REFERENCES  
 Genoscope.  
 Direct Submision  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.  
 FEATURES  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CSOD1012YJ24"  
 /issue\_type="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"  
 ORIGIN  
 Query Match 99.8%; Score 977.4; DB 4; Length 1033;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 1 GGACGCTTGCCAGCGGCGCGCCGACCCCTGACACATGACCCCGCTCGCCCTCG 60  
 |||||

DB 32 GGAAGCTTGGCCAGCGGCGCGCCGACCCCTGACACATGACCCCGCTCGCCCTCG 91  
 QY 61 GGGTGTGCAATCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTGACGAGC 120  
 DB 92 GGGTGTGCAATCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTGACGAGC 151  
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 DB 212 TACTTCTCCGTTACTACGACAGGTAACGACAGAGCTCCGCACTTCTGTACGCGG 271  
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 DB 272 GGTGGAAGGCAAGCCCAATTTCTACCTGTGAGGCTTGGAGATGCTTGTGCA 331  
 QY 301 GGAATGAAAAAGTTCCCAAGTTTCCGAGCTGCAAGTATGAGACCAAGTGTGAGG 360  
 DB 332 GGAATGAAAAAGTTCCCAAGTTTCCGAGCTGCAAGTATGAGACCAAGTGTGAGG 391  
 QY 361 GGTCCACAGAAAAGTATTTCTTAAATCTAAGTTCATGACATGTGAAAAATCTTTCCG 420  
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 DB 512 TCTGGGCAACAAAAGAAATTCATCATTTTGTCTACAGTCCAAAAGATGAGGAGCTGTCT 571  
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 QY 901 TTTATATATATACAGCTGCTATTCAAATGAGTCTACCATTTTATATATATGTTCAAC 960  
 DB 932 TTTATATATATACAGCTGCTATTCAAATGAGTCTACCATTTTATATATATGTTCAAC 991  
 QY 961 TGTTTGTGAGACTGAATTC 979  
 DB 992 TGTTTGTGAGACTGAATTC 1010  
 RESULT 9  
 CR61201 1034 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CSOD1075YM02 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).  
 ACCESSION CR61201

VERSION CR601201.1 GI:50482008  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 1034)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Parade Avenue  
2 (bases 1 to 1034)  
REFERENCE Genoscope.  
AUTHORS Direct Submision  
TITLE Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source  
Location/Qualifiers  
1..1034  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1075YM02"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 99.8%; Score 977.4; DB 4; Length 1034;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGAGCCCTTCCAGCGGCGCCCGACCCCTGACACATGAGACCCCGTCCGCCCTTGG 60  
DB 37 GGAACCCCTTGGCCAGCGGCGCCCGACCCCTGACACATGAGACCCCGTCCGCCCTTGG 96  
QY 61 GCGCTGCATTTCTGCTCTTTCTCTGACGAGGCTGACATGCTGCTGCTGACAGAC 120  
DB 97 GCGCTGCATTTCTGCTCTTTCTCTGACGAGGCTGACATGCTGCTGCTGACAGAC 156  
QY 121 CAACGAGAAATACCGGAGATCTGCTCTTCCCTTACATACGAGACCTTCCCGGCGCC 180  
DB 157 CAACGAGAAATACCGGAGATCTGCTCTTCCCTTACATACGAGACCTTCCCGGCGCC 216  
QY 181 TACTTCTCCGTTACTACTACGACAGGTACACGACAGGTGCGCCGATTCCTGTACGAGG 240  
DB 217 TACTTCTCCGTTACTACTACGACAGGTACACGACAGGTGCGCCGATTCCTGTACGAGG 276  
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DB 277 GGTGCGAGGCGCAACGCAAAATTTCTACACCTGGAGGCTTGCAGCATGCTTGTCTGGA 336  
QY 301 GGATGAGAAATGTTCCCAAGTTTCCGCGCTGACAGTGAAGTGAACGACGAGTGAAG 360  
DB 337 GGATGAGAAATGTTCCCAAGTTTCCGCGCTGACAGTGAAGTGAAGTGAAGTGAAG 396  
QY 361 GGTGCGAGGCGCAACGCAAAATTTCTTAAATCTAAAGTTCCATGATGAAATTTCTTTCCG 420  
DB 397 GGTGCGAGGCGCAACGCAAAATTTCTTAAATCTAAAGTTCCATGATGAAATTTCTTTCCG 456  
QY 421 GTGGGTGTCACCGGAAACCGAATTTGAGAACAGGTTTTCAGATGAAGTACTTGTATGGGCT 480  
DB 457 GTGGGTGTCACCGGAAACCGAATTTGAGAACAGGTTTTCAGATGAAGTACTTGTATGGGCT 516  
QY 481 TGTGGGCAACCAAGAAATTTCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGT 540

DB 517 TGTGGGCAACCAAGAAATTTCAATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGT 576  
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QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCCAAGCTTCGCTTGCAGTAGAATCC 720  
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QY 781 GGTATTTGCTTTATGTTGTATCTGAAGATTAATATGACAGCATGAGAAACATCA 840  
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QY 901 TTTATATATTAATTAAGTCTATTTCAATATGATGATACATTTTATTTATGTTCAAC 960  
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QY 961 TGTGTTGTGAGACTGAATTC 979  
DB 997 TGTGTTGTGAGACTGAATTC 1015  
RESULT 10  
CR618958  
LOCUS CR618958 1038 bp mRNA linear HTC 21-JUL-2004  
DEFINITION Full-length cDNA clone CSOD1058YM18 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION CR618958  
VERSION CR618958.1 GI:50499765  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 1038)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Parade Avenue  
2 (bases 1 to 1038)  
REFERENCE Genoscope.  
AUTHORS Direct Submision  
TITLE Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source  
Location/Qualifiers  
1..1038  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1058YM18"  
/tissue\_type="Placenta Cot 25-normalized"

ORIGIN /plasmid="pCMVSPORT\_6"

Query Match 99.8%; Score 977.4; DB 4; Length 1038;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG  
 20 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG  
 61 GGCTGCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGCGGCAATGCTGCTCAGAGAC  
 80 GGCTGCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGCGGCAATGCTGCTCAGAGAC  
 121 CAACAGAAATACCGGAGATCTGCTCTGCGCCCTGACATGACGACCCCTGCGGCGCC  
 140 CAACAGAAATACCGGAGATCTGCTCTGCGCCCTGACATGACGACCCCTGCGGCGCC  
 181 TACTCTCGCTTACTACTACGAGGTACGAGGAGCTGCGGCGGCTTCTGTAAGGAG  
 200 TACTCTCGCTTACTACTACGAGGTACGAGGAGCTGCGGCGGCTTCTGTAAGGAG  
 241 GCTGCGAGGCAACGCGCAAAATTTCTACACCTGGAGGCTTGCAGCATGCTTGGTGA  
 260 GCTGCGAGGCAACGCGCAAAATTTCTACACCTGGAGGCTTGCAGCATGCTTGGTGA  
 301 GGATGAGAAATAGTCTCCCAAGTTTGGCGCTGCAAGTGTGACGACGACGATGAGG  
 320 GGATGAGAAATAGTCTCCCAAGTTTGGCGCTGCAAGTGTGACGACGACGATGAGG  
 361 GGTCACAGAAATAGTCTTCTTAATCTAAGTTCATGACATGTGAAATTTCTTTCCG  
 380 GGTCACAGAAATAGTCTTCTTAATCTAAGTTCATGACATGTGAAATTTCTTTCCG  
 421 GTGGGTGTACCGGAAACCGATTTGAGACAGGTTTCCAGATGAGAGTCTTGTATGAG  
 440 GTGGGTGTACCGGAAACCGATTTGAGACAGGTTTCCAGATGAGAGTCTTGTATGAG  
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 500 TCTGGCGCAACAAAGAAATTTCCATCTTTTGTGACAGTCCAAAGATGAGGAGCTGT  
 541 CTGCGCAATGCACTGCTATTTAATCCAGATGAGAGCTGATGAGTCTTCACT  
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 601 ATACTGCTGTGAGGAGATGACATATACCTTTGAGAGGAGATGCAACGTCAT  
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 721 GGAATATTTGGAAGAGCAATTTAAACATTTTATATGATCTTTGTTGCTTAAAG  
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 781 GCTATTTGCTTTATGTTGTTATCTGAAGATATATGACAGATGAGGAAACAAATCA  
 800 GCTATTTGCTTTATGTTGTTATCTGAAGATATATGACAGATGAGGAAACAAATCA  
 841 TTGTGATTTATTTACCAAGTTTATTAATACAGTCACTTTTCAAAATTTGATTTT  
 860 TTGTGATTTATTTACCAAGTTTATTAATACAGTCACTTTTCAAAATTTGATTTT  
 901 TTATATATATACAGTGCATTTCAATGATGATGATGATGATGATGATGATGATGATGAT  
 920 TTATATATATACAGTGCATTTCAATGATGATGATGATGATGATGATGATGATGATGAT  
 961 TTGTTGAGACTGAATTC 979

Db 980 TGTGAGACTGAATTC 998

RESULT 11  
 CR624861 1039 bp mRNA linear HTC 21-JUL-2004  
 LOCUS full-length cDNA clone CS0D1016YN22 of Placenta Cot 25-normalized  
 DEFINITION of Homo sapiens (human).  
 ACCESSION CR624861  
 VERSION CR624861.1 GI:50505668  
 KEYWORDS HTC; CNSIT\_cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo  
 1 (bases 1 to 1039)  
 Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 Contract : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 1039)  
 Genoscope.  
 Direct Submission  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen  
 Location/Qualifiers  
 source 1..1039  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1016YN22"  
 /library="Placenta Cot 25-normalized"  
 /plasmid="pCMVSPORT\_6"

ORIGIN

Query Match 99.8%; Score 977.4; DB 4; Length 1039;  
 Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
 Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG  
 29 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG  
 61 GGCTGCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGCGGCAATGCTGCTCAGAGAC  
 89 GGCTGCAATTCCTGCTGCTTTTCTGACGAGGCTGCACTGCGGCAATGCTGCTCAGAGAC  
 121 CAACAGAAATACCGGAGATCTGCTCTGCGCCCTGACATGACGACCCCTGCGGCGCC  
 149 CAACAGAAATACCGGAGATCTGCTCTGCGCCCTGACATGACGACCCCTGCGGCGCC  
 181 TACTCTCGCTTACTACTACGAGGTACGAGGAGCTGCGGCGGCTTCTGTAAGGAG  
 209 TACTCTCGCTTACTACTACGAGGTACGAGGAGCTGCGGCGGCTTCTGTAAGGAG  
 241 GCTGCGAGGCAACGCGCAAAATTTCTACACCTGGAGGCTTGCAGCATGCTTGGTGA  
 269 GCTGCGAGGCAACGCGCAAAATTTCTACACCTGGAGGCTTGCAGCATGCTTGGTGA  
 301 GGATGAGAAATAGTCTCCCAAGTTTGGCGCTGCAAGTGTGACGACGACGATGAGG  
 329 GGATGAGAAATAGTCTCCCAAGTTTGGCGCTGCAAGTGTGACGACGACGATGAGG  
 361 GGTCACAGAAATAGTCTTCTTAATCTAAGTTCATGACATGTGAAATTTCTTTCCG 420

Db 389 GGTCCAGAAAAGATTTCTTAATCTAAGTCCAGATGTGAAAAATCTTTTCG 448  
Qy 421 GTGGGTGTACCGGAACCGGATTTGAGAACAGGTTTCCAGATGAATCTATGATGGCT 480  
Db 449 GTGGGTGTACCGGAACCGGATTTGAGAACAGGTTTCCAGATGAATCTATGATGGCT 508  
Qy 481 TCTGGCAGCAAGAAAGAAATTCATCTTTTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540  
Db 509 TCTGGCAGCAAGAAAGAAATTCATCTTTTCTACAGTCCAAAAGATGAGGAGCTGTGCT 568  
Qy 541 CTGGCAATGTGACTGCTATTTATTTAATCCAGATGAGAACTGTGATGCTTTCACCT 600  
Db 569 CTGGCAATGTGACTGCTATTTAATTTAATCCAGATGAGAACTGTGATGCTTTCACCT 628  
Qy 601 ATACTGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGATTCGAAACGTGAT 660  
Db 629 ATACTGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGATTCGAAACGTGAT 688  
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGCAGTAGAATCC 720  
Db 689 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGCAGTAGAATCC 748  
Qy 721 GGAATAATGTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTTGTCTTATG 780  
Db 749 GGAATAATGTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTTGTCTTATG 808  
Qy 781 GCTAATTTGCTTTAATGTTGTATCTGAAGAAATTAATATGACAGATGAGAAACAAATCA 840  
Db 809 GCTAATTTGCTTTAATGTTGTATCTGAAGAAATTAATATGACAGATGAGAAACAAATCA 868  
Qy 841 TTGGTGATTTATTCACCAAGTTTATTAATTAACAGTCACTTTTCAAAAATTTGATTT 900  
Db 869 TTGGTGATTTATTCACCAAGTTTATTAATTAACAGTCACTTTTCAAAAATTTGATTT 928  
Qy 901 TTATATATATATAGTGTGATTTCAAAATGTGATGCTACATTTTATTAATGTTTCAAC 960  
Db 929 TTATATATATATAGTGTGATTTCAAAATGTGATGCTACATTTTATTAATGTTTCAAC 988  
Qy 961 TGTGTGTGAGACTGAATTC 979  
Db 989 TGTGTGTGAGACTGAATTC 1007

RESULT 12  
CR621074 1042 bp mRNA linear HNC 21-JUL-2004  
LOCUS Full-length cDNA clone CS0D1012YA05 of Placenta Cot 25-normalized  
DERIVATION CR621074  
ACCESSION CR621074.1 GI:50501881  
VERSION HNC; CDSLT CDNA.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 1042)  
REFERENCE AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradise Avenue  
2 (bases 1 to 1042)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
COMMENT Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
source 1..1042  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1012YA05"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

Query Match 99.8%; Score 977.4; DB 4; Length 1042;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAAGCCCTTGCCAGCGGCGCGCCGACCCCTGACATGGAACCCGCTGCGCCCTGCG 60  
Db 37 GGAAGCCCTTGCCAGCGGCGCGCCGACCCCTGACATGGAACCCGCTGCGCCCTGCG 96  
Qy 61 GGCTGTGATTCGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 120  
Db 97 GGCTGTGATTCGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGAC 156  
Qy 121 CAACGAAATPACGGGAGATGTGTCTGTGCCCCCTAGACTACGAACTTCCGCGGCC 180  
Db 157 CAACGAAATPACGGGAGATGTGTCTGTGCCCCCTAGACTACGAACTTCCGCGGCC 216  
Qy 181 TACTTTCGGTATCTACATGACAGGTACAGGAGAGTGGCCGACATTCCTGTACGGGG 240  
Db 217 TACTTTCGGTATCTACATGACAGGTACAGGAGAGTGGCCGACATTCCTGTACGGGG 276  
Qy 241 GCTGCGAGGAGACGCCCAATTTCTTACCTGGGAGGCTTGCAGCATGCTTCTGGA 300  
Db 277 GCTGCGAGGAGACGCCCAATTTCTTACCTGGGAGGCTTGCAGCATGCTTCTGGA 336  
Qy 301 GGATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAATGTGAGCAACAGTGAAG 360  
Db 337 GGATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAATGTGAGCAACAGTGAAG 396  
Qy 361 GGTCACAGAAAGATTTCTTTAATCAATTCATGCAATGCAATGCAATTTCTTTTCG 420  
Db 397 GGTCACAGAAAGATTTCTTTAATCAATTCATGCAATGCAATGCAATTTCTTTTCG 456  
Qy 421 GTGGGTGTACCGGAACCGGATTTGAGAACAGGTTTCCAGATGAATCTATGAGGCT 480  
Db 457 GTGGGTGTACCGGAACCGGATTTGAGAACAGGTTTCCAGATGAATCTATGAGGCT 516  
Qy 481 TCTGGCAGCAAGAAAGAAATTCATCTTTTCTACAGTCCAAAAGATGAGGAGCTGTGCT 540  
Db 517 TCTGGCAGCAAGAAAGAAATTCATCTTTTCTACAGTCCAAAAGATGAGGAGCTGTGCT 576  
Qy 541 CTGGCAATGTGACTGCTATTTAATTTAATCCAGATGAGAACTGTGATGCTTTCACCT 600  
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Qy 601 ATACTGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGATTTGCAAAACGTGAT 660  
Db 637 ATACTGCTGTGAGGGAATGACAAATACCTTTGTAGCAGGAGATTTGCAAAACGTGAT 696  
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGCAGTAGAATCC 720  
Db 697 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAGCTTGTGCTTGCAGTAGAATCC 756  
Qy 721 GGAATAATGTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTTGTCTTATG 780  
Db 757 GGAATAATGTGGAAGAGCAATTTTAACTCTTAATATGTCATCTTTTGTCTTATG 816  
Qy 781 GCTAATTTGCTTTAATGTTGTATCTGAAGAAATTAATATGACAGATGAGAAACAAATCA 840  
Db 817 GCTAATTTGCTTTAATGTTGTATCTGAAGAAATTAATATGACAGATGAGAAACAAATCA 876  
Qy 841 TTGGTGATTTATTCACCAAGTTTATTAATTAACAGTCACTTTTCAAAAATTTGATTT 900

|||||  
Db 877 TTGGGATTATTCACCAAGTTTATATACAGCTTTTAAAAATTGATTT 936  
Oy 901 TTTATATTAATCTACTGCTATTTCAAAAGTGAGTCTACATTTTATTAAGTTCAAC 960  
Db 937 TTTATATTAATCTACTGCTATTTCAAAAGTGAGTCTACATTTTATTAAGTTCAAC 996  
Oy 961 TGTGTGAGACTGAATTC 979  
Db 997 TGTGTGAGACTGAATTC 1015

RESULT 13  
CR611856 1046 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CS0DI073YH22 of Placenta Cot 25-normalized  
DEFINITION  
ACCESSION CR611856  
VERSION CR611856.1 GI:50492663  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1046)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue

REFERENCE 2 (bases 1 to 1046)  
AUTHORS Genoscope.  
TITLE Direct Submision  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source location/Qualifiers  
1..1046  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DI073YH22"  
/issue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

ORIGIN  
Query Match 99.8%; Score 977.4; DB 4; Length 1046;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243; Indels 0; Gaps 0;  
Matches 978; Conservative 0; Mismatches 1;

1 GGAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 60  
2 GGAAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACACATGACCCCGCTGCGCCCTGG 91  
3 GGCTGTGATTTGCTGCTCTTTCTGACGAGAGCTGCACTGGGGCGATGCTGCTCAGAGC 120  
4 GGCTGTGATTTGCTGCTCTTTCTGACGAGAGCTGCACTGGGGCGATGCTGCTCAGAGC 151  
5 GAGCGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGGGCC 180  
6 CAACGAGAAATACGCGAGATCTGCTCTGCGCCCTAGACTACGAGACCTGCGCGGGGCC 211  
7 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCGCGAGTTCTGTACGAGG 240  
8 TACTTCTCCGTTACTACTACGACAGGTACACGAGAGCTGCGCGCGAGTTCTGTACGAGG 271

Oy 241 GCTGCGAGGGCAGACCGCAATTTCTACCTGCGAGGCTTGCAGCATCTGCTGCA 300  
Db 272 GTGCGAGGGCAGACCGCAATTTCTACCTGCGAGGCTTGCAGCATCTGCTGCA 331  
Oy 301 GATATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTATGTGACACACAGGTGAG 360  
Db 332 GATATGAAAAAGTTCCCAAGTTTCCGCGCTGCAAGTATGTGACACACAGGTGAG 391  
Oy 361 GATATGAAAAAGTTTCTTAATCTAAGTCCATGATGCAATGTAATTTCTTTCCG 420  
Db 392 GATATGAAAAAGTTTCTTAATCTAAGTCCATGATGCAATGTAATTTCTTTCCG 451  
Oy 421 GTGCGTGTACCGGACCGGATGAGACAGATTTCAGATGAGCTATGTATGGCT 480  
Db 452 GTGCGTGTACCGGACCGGATGAGACAGATTTCAGATGAGCTATGTATGGCT 511  
Oy 481 TCTGCGCACCAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 540  
Db 512 TCTGCGCACCAAGAAATTCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTCT 571  
Oy 541 CTGCGAATGTACCTCGATATTTATTCAGAGTACAGAACCTGTATGCTTCACT 600  
Db 572 CTGCGAATGTACCTCGATATTTATTCAGAGTACAGAACCTGTATGCTTCACT 631  
Oy 601 ATACTGCTGTGAGGAGATGACATATCTTTGACGAGGAGATTGCAACCTGCAT 660  
Db 632 ATACTGCTGTGAGGAGATGACATATCTTTGACGAGGAGATTGCAACCTGCAT 691  
Oy 661 GTGCAAAAGCTTTGAAAAAGAAAGAAAGATGCCAAGCTTGTGCGCAGTAGAATCC 720  
Db 692 GTGCAAAAGCTTTGAAAAAGAAAGAAAGATGCCAAGCTTGTGCGCAGTAGAATCC 751  
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Db 752 GGAATTCGAGAAAGCAATTTTAAATCTTAAATGTCACTTTTGTCTTTATG 811  
Oy 781 GCTATTTGCTTTATGTTGATCTGAAGATATATATGACAGATGAGAAACAATCA 840  
Db 812 GCTATTTGCTTTATGTTGATCTGAAGATATATATGACAGATGAGAAACAATCA 871  
Oy 841 TTGGGATTATTCACCAAGTTTATTAATCAAGTCACTTTTCAAAAATTTGATTT 900  
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Oy 901 TTTATATTAATCTACTGCTATTTCAAAAGTGAGTCTACATTTTATTAAGTTCAAC 960  
Db 932 TTTATATTAATCTACTGCTATTTCAAAAGTGAGTCTACATTTTATTAAGTTCAAC 991  
Oy 961 TGTGTGAGACTGAATTC 979  
Db 992 TGTGTGAGACTGAATTC 1010

RESULT 14  
CR605333 1047 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CS0DI075YH17 of Placenta Cot 25-normalized  
DEFINITION  
ACCESSION CR605333  
VERSION CR605333.1 GI:50486140  
KEYWORDS HTC; CNSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1047)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Paradey Avenue

REFERENCE 2 (bases 1 to 1047)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source location/Qualifiers  
1..1047  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1075B17"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 99.8%; Score 977.4; DB 4; Length 1047;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 GAAGCGCTTGGCCAGCGGCGCCCGACCCCTTGACACATGACCCCGCTGCGCCCTTGG 60  
29 GAGACGCTTGGCCAGCGGCGCCCGACCCCTTGACACATGACCCCGCTGCGCCCTTGG 88  
61 GGCTGTGCAATTCGCTGCTTCTCTGACGAGGCTGCACTGGGGCATGCTGCTGACGAGC 120  
89 GGCTGTGCAATTCGCTGCTTCTCTGACGAGGCTGCACTGGGGCATGCTGCTGACGAGC 148  
121 CAACAGAAATACCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
149 CAACAGAAATACCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 208  
181 TACTTCTCGTTACTACTACGAGGTACGAGGCTGCGCGCACTTCTGTAACGAGG 240  
209 TACTTCTCGTTACTACTACGAGGTACGAGGCTGCGCGCACTTCTGTAACGAGG 268  
241 GGTGGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGACATGCTTCTGTA 300  
269 GGTGGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGACATGCTTCTGTA 328  
301 GGATAGAAATAGTCCCAAGTTTCCCGCTGCAAGTGTGAGACGACAGTGTGAGG 360  
329 GGATAGAAATAGTCCCAAGTTTCCCGCTGCAAGTGTGAGACGACAGTGTGAGG 388  
361 GGTCACAGAAATAGTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 420  
389 GGTCACAGAAATAGTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 448  
421 GTGGGTGTCAACCGGATTTGAGAACAGGTTTCCAGATAGCTTCTGTATGGGCT 480  
449 GTGGGTGTCAACCGGATTTGAGAACAGGTTTCCAGATAGCTTCTGTATGGGCT 508  
481 TTGGGCAACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
509 TTGGGCAACCAAGAAATTTCCATCATTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 568  
541 CTGCAATGTGACTGCTATTTATTTTAAATCAAGATACAGAACTGTGATGCTTCACT 600  
569 CTGCAATGTGACTGCTATTTATTTTAAATCAAGATACAGAACTGTGATGCTTCACT 628  
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629 ATACTGCTGTGAGGAAATGACATTAATTTGTTAGACGAGGAGATTTGCAAACTGTGAT 688  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAAAGCTTGTGCTTGTGCAATGAAATCC 720  
689 GTGCAAAAGCTTTGAAAAAGAAAGATGCAAAAGCTTGTGCTTGTGCAATGAAATCC 748

721 GAAAAATCGAAGAGCAATTTTAAACTTTAATATGTCANCTGTTGCTTTATG 780  
749 GAAAAATCGAAGAGCAATTTTAAACTTTAATATGTCANCTGTTGCTTTATG 808  
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809 GCTTATTTGCTTTATGTTGTTATCTGAAGATATATAGACATGAGAAACAATCA 868  
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LOCUS Full-length cDNA clone CSOD1067A08 of Placenta Cot 25-normalized  
DEFINITION of Homo sapiens (human).  
ACCESSION CR607266  
VERSION CR607266.1 GI:50488073  
KEYWORDS HTC; CNSIT. cDNA.  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1050)  
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
CONTACT Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 1050)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
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Query Match 99.8%; Score 977.4; DB 4; Length 1050;  
Best Local Similarity 99.9%; Pred. No. 1.6e-243;  
Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
1 GAAGCGCTTGGCCAGCGGCGCCCGACCCCTTGACACATGACCCCGCTGCGCCCTTGG 60  
36 GAGACGCTTGGCCAGCGGCGCCCGACCCCTTGACACATGACCCCGCTGCGCCCTTGG 95  
61 GGCTGTGCAATTCGCTGCTTCTCTGACGAGGCTGCACTGGGGCATGCTGCTGACGAGC 120  
96 GGCTGTGCAATTCGCTGCTTCTCTGACGAGGCTGCACTGGGGCATGCTGCTGACGAGC 155



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Search completed: March 11, 2006, 08:20:02  
Job time : 4768 secs



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NAME/KEY: CDS  
LOCATION: 39..746  
US-08-147-710-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.8e-264; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGCTGTGATTTCTGCTGCTTTCTGACGAGAGCTGCACTGGCCGATGCTGCTCAGAGC 120  
QY 121 CAACAGAAATACGCGAGATCTGTCTCTGCGCCCTAGACTACGGAACCTGCGGGGCC 180  
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QY 181 TACTTCTCGTTACTACTACGAGGTACAGAGGTACGAGAGGTGCGCGGCTTCTGTACGGGG 240  
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DB 961 TGTGTTGAGACTGAATTC 979

RESULT 2

US-08-458-090-1

Sequence 1, Application US/08458090



Patent No. 5728674

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Kistler, Walter

APPLICANT: Foster, Donald C.

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND

TITLE OF INVENTION: METHODS RELATING THERETO

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: ZymoGenetics, Inc.

STREET: 1201 Baseline Avenue East

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,090

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary B

REGISTRATION NUMBER: 31-648

REFERENCE/DOCKET NUMBER: 93-14D2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6673

TELEFAX: 206-442-6678

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 979 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: Placenta

IMMEDIATE SOURCE:

CLONE: J-2-11

FEATURES:

NAME/KEY: CDS

LOCATION: 39..746

US-08-458-090-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
Best Local Similarity 100.0%; Pred. No. 1.8e-264; Indels 0; Gaps 0;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
 US-08-457-887-1



/ Sequence 1, Application US/08457887  
 / Patent No. 5914315  
 / GENERAL INFORMATION:  
 / APPLICANT: Sprecher, Cindy A.  
 / APPLICANT: Kiesel, Walter  
 / APPLICANT: Foster, Donald C.  
 / TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND  
 / TITLE OF INVENTION: METHODS RELATING THEREIN  
 / NUMBER OF SEQUENCES: 15  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSES: ZymoGenetics, Inc.  
 / STREET: 1201 Bablake Avenue East  
 / CITY: Seattle  
 / STATE: WA  
 / COUNTRY: USA  
 / ZIP: 98102

/ COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent Release #1.0, Version #1.25  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/457,887  
 / FILING DATE:  
 / CLASSIFICATION: 536  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Parker, Gary B  
 / REGISTRATION NUMBER: 31-648  
 / REFERENCE/DOCKET NUMBER: 93-14D1  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 206-442-6673  
 / TELEFAX: 206-442-6678  
 / INFORMATION FOR SEQ ID NO: 1:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 979 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: double  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: cDNA  
 / ORIGINAL SOURCE:  
 / ORGANISM: Homo sapiens  
 / TISSUE TYPE: Placenta  
 / IMMEDIATE SOURCE:  
 / CLONE: J-2-11  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: 39..746  
 / US-08-457-887-1

Query Match 100.0%; Score 979; DB 2; Length 979;  
 Best Local Similarity 100.0%; Pred. No. 1,8e-264; Indels 0; Gaps 0;  
 Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 GGTGTGATCTGTCTGTTTCTGACGAGGCTGCACTGGGAGTCTCTCAGAGC 120  
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Qy	781	GCTTATTTGCTTATATGTTGTATCTGAAGATTAATATGACAGTATGAGAAACAAATCA	840
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Db	961	TGTTTGTGAGACTGAATTC	979

RESULT 4  
US-09-016-434-1378  
Sequence 1378, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Sellmeier  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ. ID NO: 1378:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 979 base pairs

claim  
plurality

claim  
plurality of probos  
1-1480

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; CLONE: g441149
;
US-09-016-434-1378

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Best Local Similarity	100.0%;	Pred. No. 1.8e-264;		
Matches 979; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Db	241	GCTGCGAGGGCAACGCGCAATTTCTACCTGGGAGGCTTGGCGACGATGCTGCTGCGA	300
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Db	361	GGGCCACAGAAAAGTATTTCTTTATCTCAATTCACAGACATGAGAAAATTCCTTTCCG	420
QY	421	GTCGCGTGTCAACCGGAACCGGATTTGAGAACAGTTTCCAGATGAAGCTATGTAGGGCT	480
Db	421	GTCGCGTGTCAACCGGAACCGGATTTGAGAACAGTTTCCAGATGAAGCTATGTAGGGCT	480
QY	481	TCGCGGCACAAAAGAAAATTCATCATTTTGTGCTACAGTCCAAAAGATGAGGAGCTGTGCT	540
Db	481	TCGCGGCACAAAAGAAAATTCATCATTTTGTGCTACAGTCCAAAAGATGAGGAGCTGTGCT	540
QY	541	CTGCGCAATGTACTGCTGATTTATTTTAACTCCAATACAGAACTGTGATGCTTTCACT	600
Db	541	CTGCGCAATGTACTGCTGATTTATTTTAACTCCAATACAGAACTGTGATGCTTTCACT	600
QY	601	ATATCTGCGTGTGAGAGGAATGACATTAATCTTGTAGACGAGAGATGCGAAACGTGCAT	660
Db	601	ATATCTGCGTGTGAGAGGAATGACATTAATCTTGTAGACGAGAGATGCGAAACGTGCAT	660
QY	661	GTCGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAAGCTTCGTTTCCAGTAGAATCC	720
Db	661	GTCGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAAGCTTCGTTTCCAGTAGAATCC	720
QY	721	GGAAAATTGCGAAGAGCAATTTTAACATCTTTAATATGTCACTCTGTTGTCTTATG	780
Db	721	GGAAAATTGCGAAGAGCAATTTTAACATCTTTAATATGTCACTCTGTTGTCTTATG	780
QY	781	GGCTAATTTGCGTTATGTTGATCTGAGAAATAATGACAGATAGAGAAACAATCA	840
Db	781	GGCTAATTTGCGTTATGTTGATCTGAGAAATAATGACAGATAGAGAAACAATCA	840
QY	841	TTGCGTATTTTACCAAGTTTATTTAATACAGTCACTTTTCAAAAAATTGGAATTT	900
Db	841	TTGCGTATTTTACCAAGTTTATTTAATACAGTCACTTTTCAAAAAATTGGAATTT	900
QY	901	TTTATATATTAACACTGCTGCTATTCAAATGAGTCTCAATTTTAAATTTATGCTTCAAC	960
Db	901	TTTATATATTAACACTGCTGCTATTCAAATGAGTCTCAATTTTAAATTTATGCTTCAAC	960

Db 901 TTTATATATACAGCTGCTATTCATATGATGATCTACATTTTATTTATGTTCAAC 960  
Qy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

RESULT 5  
US-09-904-621-1

Sequence 1, Application US/09904621  
Patent No. 6656746  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kistler, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/09/904,621  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: EARLIER FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39)...(746)  
US-09-904-621-1

Query Match 100.0%; Score 979; DB 3; Length 979;

Best Local Similarity 100.0%; Pred. No. 1,86-264; Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGACATGAGACCCCGCTGCGCCCTGAG 60  
Db 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGACATGAGACCCCGCTGCGCCCTGAG 60  
Qy 61 GAGTGTGATTCGTGCTGCTTTCTGACGAGAGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Db 61 GAGTGTGATTCGTGCTGCTTTCTGACGAGAGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Qy 121 CAACGAGAAATACCGCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Db 121 CAACGAGAAATACCGCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Qy 181 TACTTCTCGTACTACTACGACAGATCAAGCAGAGCTGCGCGAGTCTGCTGCTGCTGCTGCT 240  
Db 181 TACTTCTCGTACTACTACGACAGATCAAGCAGAGCTGCGCGAGTCTGCTGCTGCTGCTGCT 240  
Qy 241 GCTGCGAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTTGCAGAG 300  
Db 241 GCTGCGAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTTGCAGAG 300  
Qy 301 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 360  
Db 301 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 360  
Qy 361 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 420  
Db 361 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 420  
Qy 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCAAGTGAAGTGAAGTGAAGTGAAG 480  
Db 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCAAGTGAAGTGAAGTGAAGTGAAG 480

Qy 481 TCTGCGACCAAGAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
Db 481 TCTGCGACCAAGAAATTCATCTTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
Qy 541 CTGCGCAATGTGACTGCTATTTATTTATTCAGATACAGAACTGTGAGTCTTCACT 600  
Db 541 CTGCGCAATGTGACTGCTATTTATTTATTCAGATACAGAACTGTGAGTCTTCACT 600  
Qy 601 ATACTGCTGTGAGGAGAAATCAATTAATTTTACAGGAGAGATTTGCAAGTGTGAT 660  
Db 601 ATACTGCTGTGAGGAGAAATCAATTAATTTTACAGGAGAGATTTGCAAGTGTGAT 660  
Qy 661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCAAGTCTGCTTGCAGTGAATTC 720  
Db 661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCAAGTCTGCTTGCAGTGAATTC 720  
Qy 721 GAAATTCGAGAGACCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 780  
Db 721 GAAATTCGAGAGACCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 780  
Qy 781 GCTATTTGCTTTATGCTTTATCTGAGATTAATTAATTAATTAATTAATTAATTAATTA 840  
Db 781 GCTATTTGCTTTATGCTTTATCTGAGATTAATTAATTAATTAATTAATTAATTAATTA 840  
Qy 841 TTGGGATTTATTCACGAGTCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 900  
Db 841 TTGGGATTTATTCACGAGTCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 900  
Qy 901 TTTATATATACAGCTGCTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 960  
Db 901 TTTATATATACAGCTGCTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 960  
Qy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

RESULT 6

US-09-949-016-1187

Sequence 1187, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1187  
LENGTH: 1583  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-1187

Query Match 99.8%; Score 977.4; DB 3; Length 1583;

Best Local Similarity 99.9%; Pred. No. 6,4e-264; Matches 978; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGACATGAGACCCCGCTGCGCCCTGAG 60  
Db 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGACATGAGACCCCGCTGCGCCCTGAG 60  
Qy 61 GAGTGTGATTCGTGCTGCTTTCTGACGAGAGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Db 61 GAGTGTGATTCGTGCTGCTTTCTGACGAGAGCTGCACTGCGGAGTCTGCTGAGAGC 120  
Qy 121 CAACGAGAAATACCGCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Db 121 CAACGAGAAATACCGCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
Qy 181 TACTTCTCGTACTACTACGACAGATCAAGCAGAGCTGCGCGAGTCTGCTGCTGCTGCTGCT 240  
Db 181 TACTTCTCGTACTACTACGACAGATCAAGCAGAGCTGCGCGAGTCTGCTGCTGCTGCTGCT 240  
Qy 241 GCTGCGAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTTGCAGAG 300  
Db 241 GCTGCGAGGCAACGCAATTTCTACCTGAGAGGCTTGCAGAGATGCTTGCAGAG 300  
Qy 301 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 360  
Db 301 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 360  
Qy 361 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 420  
Db 361 GATGAGAAAGTTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACGAGTGAAG 420  
Qy 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCAAGTGAAGTGAAGTGAAGTGAAG 480  
Db 421 GTGGGTGTCAACGAGACCGGATGAGACAGGTTTCAAGTGAAGTGAAGTGAAGTGAAG 480

121 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 180  
139 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 198  
181 TACTCTCCGTTACTACTACGACAGGTACAGCAGAGCGCGCGCGAGTTCCGTACGAGG 240  
199 TACTCTCCGTTACTACTACGACAGGTACAGCAGAGCGCGCGAGTTCCGTACGAGG 258  
241 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTGCAGCAGTGTCTGCA 300  
259 GCTGCGAGGCGCAACGCAATTTCTACCTGTGAGGCTTGCAGCAGTGTCTGCA 318  
301 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAACAACAAGTGTGAG 360  
319 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAACAACAAGTGTGAG 378  
361 GGTCCACAGAAAAGTATTTCTTATCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 420  
379 GGTCCACAGAAAAGTATTTCTTATCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 438  
421 GTGGGTGTACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAAGCTACTGTATGAGCT 480  
439 GTGGGTGTACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAAGCTACTGTATGAGCT 498  
481 TCTGGCGACCAAGAAAATTCATATTTGCTACAGTCCAAAAGATGAGGAGCTGTCT 540  
499 TCTGGCGACCAAGAAAATTCATATTTGCTACAGTCCAAAAGATGAGGAGCTGTCT 558  
541 CTGCGCAATGTACCTGCTATTTATTTATCCAAAGTACAGAACTGTATGCTTTCACT 600  
559 CTGCGCAATGTACCTGCTATTTATTTATCCAAAGTACAGAACTGTATGCTTTCACT 618  
601 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGAGGAGGAGATTGCAAACTGTGAT 660  
619 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGAGGAGGAGATTGCAAACTGTGAT 678  
661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTGCCTTGCAGTAGAATCC 720  
679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTGCCTTGCAGTAGAATCC 738  
721 GGAATAATCGAAGAAAGCAATTTTAACATCTTAAATGATGATCTTGTGTCTTTATG 780  
739 GGAATAATCGAAGAAAGCAATTTTAACATCTTAAATGATGATCTTGTGTCTTTATG 798  
781 GCTTATTTGCTTTATGTTGTTGATCTGAAGATTAATATGACAGATGAGAAAACAATCA 840  
799 GCTTATTTGCTTTATGTTGTTGATCTGAAGATTAATATGACAGATGAGAAAACAATCA 858  
841 TTGATGATTTATTCACAGATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 900  
859 TTGATGATTTATTCACAGATTTTATTAATACAGTCACTTTTCAAAAATTTGATTTT 918  
901 TTTAATATTAATCTACTGCTATCAAAATGTAGTACATTTTAAATTTATGTTTAC 960  
919 TTTAATATTAATCTACTGCTATCAAAATGTAGTACATTTTAAATTTATGTTTAC 978  
961 TGTGTGAGACTGAATTC 979  
979 TGTGTGAGACTGAATTC 997

## RESULT 7

US-09-949-016-864

; Sequence 864, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

;; PRIOR APPLICATION NUMBER: 60/241,755  
;; PRIOR FILING DATE: 2000-10-20  
;; PRIOR APPLICATION NUMBER: 60/237,768  
;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 864  
;; LENGTH: 1142  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-864

Query Match 99.3%; Score 972.2; DB 3; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.6e-262;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 GGAAGCCTTGGCCGAGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCCCCCTGG 60  
19 GGAAGCCTTGGCCGAGGCGCGCGCCGACCCCTGACACATGAGACCCCGCTGCCCCCTGG 78  
61 GGCTGTGATTTCTGCTCTTTTCTGACGAGGCTGCACTGAGGATGCTCTCAGAGAC 120  
79 GGCTGTGATTTCTGCTCTTTTCTGACGAGGCTGCACTGAGGATGCTCTCAGAGAC 138  
121 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 180  
139 CAACGAGAAATACGCGGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTCCGCGGCC 198  
181 TACTCTCCGTTACTACTACGACAGGTACAGCAGAGCGCGCGAGTTCCGTACGAGG 240  
199 TACTCTCCGTTACTACTACGACAGGTACAGCAGAGCGCGCGAGTTCCGTACGAGG 258  
241 GCTGCGAGGCGCAACGCAATTTCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 300  
259 GCTGCGAGGCGCAACGCAATTTCTAAGTTCATGACATGTAAGAAAATTTCTTTCCG 318  
301 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAACAACAAGTGTGAG 360  
319 GGATGAGAAAAGTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAACAACAAGTGTGAG 378  
361 GGTCCACAGAAAAGTATTTCTTAAATCTTAAATGATGATCTTGTGTCTTTATG 420  
379 GGTCCACAGAAAAGTATTTCTTAAATCTTAAATGATGATCTTGTGTCTTTATG 438  
421 GTGGGTGTACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAAGCTACTGTATGAGCT 480  
439 GTGGGTGTACCGGAAACCGGATTTGAGAACAGGTTCCAGATGAAGCTACTGTATGAGCT 498  
481 TCTGCGACCAAGAAAATTCATATTTGCTACAGTCCAAAAGATGAGGAGCTGTCT 540  
499 TCTGCGACCAAGAAAATTCATATTTGCTACAGTCCAAAAGATGAGGAGCTGTCT 558  
541 CTGCGCAATGTACCTGCTATTTATTTATCCAAAGTACAGAACTGTATGCTTTCACT 600  
559 CTGCGCAATGTACCTGCTATTTATTTATCCAAAGTACAGAACTGTATGCTTTCACT 618  
601 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGAGGAGGAGATTGCAAACTGTGAT 660  
619 ATACTGCTGTGAGGAGATGACATTAATCTTGTAGAGGAGGAGATTGCAAACTGTGAT 678  
661 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTGCCTTGCAGTAGAATCC 720  
679 GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCCAAAGCTTGCCTTGCAGTAGAATCC 738  
721 GGAATAATCGAAGAAAGCAATTTTAACATCTTAAATGATGATCTTGTGTCTTTATG 780  
739 GGAATAATCGAAGAAAGCAATTTTAACATCTTAAATGATGATCTTGTGTCTTTATG 798  
781 GCTTATTTGCTTTATGTTGTTGATCTGAAGATTAATATGACAGATGAGAAAACAATCA 840  
799 GCTTATTTGCTTTATGTTGTTGATCTGAAGATTAATATGACAGATGAGAAAACAATCA 858



Qy 841 TTGGGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 900  
 Db 859 TTGGGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 918  
 Qy 901 TTTATATTAATACAGTCTATTCATTAATAGTACATTTTAAATTAATGTTCAAC 960  
 Db 919 TTTATATTAATACAGTCTATTCATTAATAGTACATTTTAAATTAATGTTCAAC 978  
 Qy 961 TTTTGTGAGACTGAAT 977  
 Db 979 TTTTGTGAGACTGAAT 995

X

*Method treat  
 of retinal disease*

RESULT 8  
 US-08-817-145-2  
 Sequence 2, Application US/08817145  
 Patent No. 6025329  
 GENERAL INFORMATION:  
 APPLICANT: UTSUMI, Jim  
 APPLICANT: SUDO, Teisuo  
 APPLICANT: TANAKA, Yasuhiko  
 APPLICANT: MATSUI, Mizuo  
 TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC  
 TITLE OF INVENTION: DISEASES  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Birch, Stewart, Kolasch & Birch, LLP.  
 STREET: P.O. Box 747  
 CITY: Falls Church  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22040-0747  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/817,145  
 FILING DATE: 02-JUL-1997  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MURPHY JR., Gerald M.  
 REGISTRATION NUMBER: 28,977  
 REFERENCE/DOCKET NUMBER: 760-230P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-205-8050  
 TELEFAX: 703-205-8050  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1140 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 49..753  
 US-08-817-145-2

Query Match 98.8%, Score 967, DB 3, Length 1140;  
 Best Local Similarity 99.9%, Pred. No. 4, 5e-261;  
 Matches 978, Conservative 0, Mismatches 0, Indels 1, Gaps 1;

Qy 1 GGAGCGCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGCCCGCTGCGCCCTGG 60  
 Db 12 GGAGCGCTTGGCCAGGCGGCGCCGACCCCTGACACATGAGCCCGCTGCGCCCTGG 70  
 Qy 61 GGCTGTGATTCGTGCTGCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAGC 120  
 Db 71 GGCTGTGATTCGTGCTGCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAGC 130

Qy 121 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTAGAGCACTTCCGCGGCC 180  
 Db 131 CAACAGAAATTAACCGGAGATCTGTCTCTGCCCCCTAGACTAGAGCACTTCCGCGGCC 190  
 Qy 181 TACTTCTCCGTTACTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 Db 191 TACTTCTCCGTTACTACTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 250  
 Qy 241 GGTGAGAGGAGCAAGCCCAATTTCTACCTGGAGGCTTGGACAGATGCTGCTGGA 300  
 Db 251 GGTGAGAGGAGCAAGCCCAATTTCTACCTGGAGGCTTGGACAGATGCTGCTGGA 310  
 Qy 301 GGATAGAAAAAGTTCCCAAGTTGCGCGCTGCAAGTATGATGATGATGATGATGATGATGAT 360  
 Db 311 GGATAGAAAAAGTTCCCAAGTTGCGCGCTGCAAGTATGATGATGATGATGATGATGATGAT 370  
 Qy 361 GGTCCACAGAAAGATTTCTTTATCTAATGATGATGATGATGATGATGATGATGATGATGAT 420  
 Db 371 GGTCCACAGAAAGATTTCTTTATCTAATGATGATGATGATGATGATGATGATGATGATGAT 430  
 Qy 421 GTGGGTGTACCGGAGCCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 480  
 Db 431 GTGGGTGTACCGGAGCCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 490  
 Qy 481 TCTGGCACCAAAAGAAATTCATCTATTTGCTACAGTCCAAAGATGAGAGAGCTGTGCT 540  
 Db 491 TCTGGCACCAAAAGAAATTCATCTATTTGCTACAGTCCAAAGATGAGAGAGCTGTGCT 550  
 Qy 541 CTGCCAATGTACTGCTATTTATTTAATCCAGATACAGAACTGTGATGCTTCACTT 600  
 Db 551 CTGCCAATGTACTGCTATTTATTTAATCCAGATACAGAACTGTGATGCTTCACTT 610  
 Qy 601 ATACTGCTGTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 Db 611 ATACTGCTGTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670  
 Qy 661 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTGCCTTCCAGTAGAATCC 720  
 Db 671 GTGCAAAAGCTTTGAAAAAGAAAGAGATGCCAAAGCTTGCCTTCCAGTAGAATCC 730  
 Qy 721 GGAATAATCGAAGAGCAATTTTAAATTTAAATGATGATGATGATGATGATGATGATGATGAT 780  
 Db 731 GGAATAATCGAAGAGCAATTTTAAATTTAAATGATGATGATGATGATGATGATGATGATGAT 790  
 Qy 781 GCTTATTTGCTTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
 Db 791 GCTTATTTGCTTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850  
 Qy 841 TTGGGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 900  
 Db 851 TTGGGATTTATTCACAGTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 910  
 Qy 901 TTTATATTAATACAGTCTATTCATTAATAGTACATTTTAAATTAATGTTCAAC 960  
 Db 911 TTTATATTAATACAGTCTATTCATTAATAGTACATTTTAAATTAATGTTCAAC 970  
 Qy 961 TTTTGTGAGACTGAATC 979  
 Db 971 TTTTGTGAGACTGAATC 989

RESULT 9  
 US-09-702-705-64  
 Sequence 64, Application US/09702705  
 Patent No. 6504010  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Tongtong  
 APPLICANT: Bangur, Chaitanya S.  
 APPLICANT: Lodes, Michael A.  
 APPLICANT: Fanger, Gary  
 APPLICANT: Vedvick, Tom  
 APPLICANT: Carter, Darlick  
 APPLICANT: Retter, Marc

```

; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(528)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-64
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Query Match      45.7%; Score 447; DB 3; Length 528;
Best Local Similarity 87.5%; Pred. No. 2.7e-115;
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;
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QY 1 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGTGACCATGAGCCCGCTGCGCCCTGG 60
DB 27 SGAGCCCTTGGCCAGGCGGCGCCGACCCCTGTGRCATGAGACCCCGCTGCGCCCTGG 86
QY 61 GGCTGTGATTCCTGCTGCTTTCTGTACGAGAGCTGCACTGCGCGATGCTGCTCAGAGC 120
DB 87 GGMTTGTATCTGCTGCTTTCTGTGRCAGAGCTGCACTGCGCGATGCTGATCARAGAC 146
QY 121 CAACGAGAAATPACGCGGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 180
DB 147 CAACGAGAAATPACRCCGAGATCTGCTCTGCCCCCTAGACTAGACCTGCGCGGCC 206
QY 181 TACTTCTCCGTACTACTACGACGATACGAGAGCTGCGCGCGATTCCTGTACGAGG 240
DB 207 TACTTCTCCGTACTACTACGAGATACGAGAGCTGCGCGCGATTCCTGTACGAGG 266
QY 241 GCTGCGAGGCGCAACGCAATTTCTACACCTGAGAGGCTTGCAGAGCTTCTGCTGGA 300
DB 267 GCTGCRABSGCAACGCAATTTCTACACCTGAGAGGCTTGCAGAGCTTCTGCTGGA 326
QY 301 GGATGAGAAAGTTCCAAAGTTGCGCGCTGCAAGTGAAGTGAAGCAACGATGAGG 360
DB 327 RGATGAGAAAGTTCCAAAGTTGCGCGCTGCAAGTGAAGTGAAGCAACGATGAGG 386
QY 361 GGTCCACGAGAAAGTATTTCTTAATCTAAGTTCATGATCAATGAGAAATTTCTTTCCG 420
DB 387 GGTACACAGATTAAGTATTTCTTAATCTAARKWCCATGACATGAGAAATTTCTTTNCG 446
QY 421 GTGGGTGTACCGGAAACCGGATTTGAGAAACAGTTTCCAGATGAAGCTACTGTATGGCT 480
DB 447 GTGGNGTCAACCGG-AACCGGATTTGAGAAACANGTTTTCAGATGANGCTACTGGATGGCT 505
QY 481 TCTGCGCACCAAGAAATTTCCA 503
DB 506 CCTGCRACANNAAGAAANTATCA 528
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RESULT 10
US-09-736-457-64
; Sequence 64, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
```

```

; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 64
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(528)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-64
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Query Match      45.7%; Score 447; DB 3; Length 528;
Best Local Similarity 87.5%; Pred. No. 2.7e-115;
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;
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QY 1 GGAAGCCCTTGGCCAGGCGGCGCCGACCCCTGTGACCATGAGCCCGCTGCGCCCTGG 60
DB 27 SGAGCCCTTGGCCAGGCGGCGCCGACCCCTGTGRCATGAGACCCCGCTGCGCCCTGG 86
QY 61 GGCTGTGATTCCTGCTGCTTTCTGTACGAGAGCTGCACTGCGCGATGCTGCTCAGAGC 120
DB 87 GGMTTGTATCTGCTGCTTTCTGTGRCAGAGCTGCACTGCGCGATGCTGATCARAGAC 146
QY 121 CAACGAGAAATPACGCGGAGATCTGTCTCTGCCCCCTAGACTAGAGACCTGCGCGGCC 180
DB 147 CAACGAGAAATPACRCCGAGATCTGCTCTGCCCCCTAGACTAGACCTGCGCGGCC 206
QY 181 TACTTCTCCGTACTACTACGACGATACGAGAGCTGCGCGCGATTCCTGTACGAGG 240
DB 207 TACTTCTCCGTACTACTACGAGATACGAGAGCTGCGCGCGATTCCTGTACGAGG 266
QY 241 GCTGCGAGGCGCAACGCAATTTCTACACCTGAGAGGCTTGCAGAGCTTCTGCTGGA 300
DB 267 GCTGCRABSGCAACGCAATTTCTACACCTGAGAGGCTTGCAGAGCTTCTGCTGGA 326
QY 301 GGATGAGAAAGTTCCAAAGTTGCGCGCTGCAAGTGAAGTGAAGCAACGATGAGG 360
DB 327 RGATGAGAAAGTTCCAAAGTTGCGCGCTGCAAGTGAAGTGAAGCAACGATGAGG 386
QY 361 GGTCCACGAGAAAGTATTTCTTAATCTAAGTTCATGATCAATGAGAAATTTCTTTCCG 420
DB 387 GGTACACAGATTAAGTATTTCTTAATCTAARKWCCATGACATGAGAAATTTCTTTNCG 446
QY 421 GTGGGTGTACCGGAAACCGGATTTGAGAAACAGTTTCCAGATGAAGCTACTGTATGGCT 480
DB 447 GTGGNGTCAACCGG-AACCGGATTTGAGAAACANGTTTTCAGATGANGCTACTGGATGGCT 505
QY 481 TCTGCGCACCAAGAAATTTCCA 503
DB 506 CCTGCRACANNAAGAAANTATCA 528
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RESULT 11
US-09-614-124B-64
; Sequence 64, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
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; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
```

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1 TITLE OR INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
2 FILE REFERENCE: 210121.478C3
3 CURRENT APPLICATION NUMBER: US/09/614,124B
4 CURRENT FILING DATE: 2001-07-11
5 NUMBER OF SEQ ID NOS: 1668
6 SOFTWARE: PASTESEQ for Windows Version 3.0
7 SEQ ID NO 64
8 LENGTH: 528
9 TYPE: DNA
10 ORGANISM: Homo sapien
11 FEATURE:
12 NAME/KEY: mlec_feature
13 LOCATION: (1)...(528)
14 OTHER INFORMATION: n = A,T,C or G
15 US-09-614-124B-64

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Query Match	45.7%	Score 447	DB 3	Length 528
Best Local Similarity	87.5%	Pred. No. 2.7e-115		
Matches 440, Conservative	42	Mismatches 20	Indels 1	Gaps 1

Oy	1	GAAGCCCTTGCCCAACGGGCGCGCCGACCCCTGACCAATGACCCCGCTGCGCCCTTG	60
Db	27	SGAGCCCTTGCCCAACGGGCGCGCCGACCCCTGACCAATGACCCCGCTGCGCCCTTG	86
Oy	61	GGCTGCGAATCTGCTGCTTTTCTGACGAGAGCTGCACTGCGAGTCTGCTCAAGAC	120
Db	87	GGMTGTGATKCTGCTGCTTTTCTGACGAGAGCTGCACTGCGCGAGTCTGATCAAGAC	146
Oy	121	CAACGGAATTAACGCGAGATCTGCTCTGCGCCCTAAGTACGACCTCTGCGCGCC	180
Db	147	CAACGGAATTAACGCGAGATCTGCTCTGCGCCCTAAGTACGACCTCTGCGCGCC	206
Oy	181	TACTCTCGTACTACTACGACGGTACACGACAGCGTCCGCGCACTTCTGTAAGG	240
Db	207	TACTTTCGGTACTACTACGACGGTACACGACAGCGTCCGCGCACTTCTGTAAGG	266
Oy	241	GCTCGAGGGCAACGCGCAACAATTTCTACACCTGAGAGCTTGCGACGATCTTGCTGA	300
Db	267	GCTGRABGGCAACGCGCAACAATTTCTACACCGKAGGTTTCGACATGCTGWSGTGA	326
Oy	301	GGATGAAAAAGTTCCTCCAAAGTTTGC CGGCTGCAAGTGAAGTGAAGCAACAATGAGG	360
Db	327	RGATGAAAAAGTTCCTCCAAAGTTTGC CGGCTGCAAGTGAAGTGAAGCAACAAGTGAAGG	386
Oy	361	GGTCAACGAAAAATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCCG	420
Db	387	GGTCAACGAGATTAAGTATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTNCG	446
Oy	421	GTGGGTGTCAACGGAAACCGGATTGAGAACAGGTTTCCAGATGAAGCTACTGTGATGGCT	480
Db	447	GTGGGNGTCAACCGG-AACGGATTTGAAGAACAGTTTGCAGATGAAGCTACTGTGATGGCT	505
Oy	481	TCTGGCACCAAGAAAAATTCCA 503	
Db	506	CTGCGCACAAAAAGAAATATCA 528	

RESULT 12  
 US-09-671-325-64  
 Sequence 64, Application US/09671325  
 Patent No. 6667154  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Tongtong  
 APPLICANT: Bangur, Chaitanya S.  
 APPLICANT: Lodes, Michael A.  
 APPLICANT: Fanger, Gary  
 APPLICANT: Vedvick, Tom  
 APPLICANT: Carter, Darick  
 APPLICANT: Retter, Marc  
 APPLICANT: Mannion, Jane  
 APPLICANT: Pan, Liqun  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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? TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.478C12
? CURRENT APPLICATION NUMBER: US/09/671,325
? CURRENT FILING DATE: 2000-09-26
? NUMBER OF SEQ ID NOS: 1825
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 64
? LENGTH: 528
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURES:
? NAME/KEY: misc feature
? LOCATION: (1)...(528)
? OTHER INFORMATION: n = A,T,C or G
US-09-671-325-64

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Query Match	45.7%	Score 447	DB 3	length 528
Best Local Similarity	87.5%	Prod. No.	2	7e-115
Matches 440	Conservative 42	Mismatches 20	Indels 1	Gaps 1

[illegible]

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RESULT 13
US-09-589-184-64
; Sequence 64, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8

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;/ CURRENT APPLICATION NUMBER: US/09/589,184  
;/ CURRENT FILING DATE: 2000-06-05  
;/ NUMBER OF SEQ ID NOS: 827  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 64  
;/ LENGTH: 528  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapien  
;/ FEATURE:  
;/ NAME/KEY: misc.feature  
;/ LOCATION: (1)...(528)  
;/ OTHER INFORMATION: n = A,T,C or G  
US-09-589-184-64

Query Match 45.7%; Score 447; DB 3; Length 528;  
Best Local Similarity 87.5%; Pred. No. 2.7e-115;  
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;

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QY 1 GGAAGCCCTTGGCCAGCGGCGCCGACCCCTGCAACATGACCCCGCTGCGCCCTGG 60
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Db 27 SGACGCCCTTGGCCAGCGGCGCCGACCCCTGSRCAATGACCCCGCTGCGCCCTGG 86
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GGCTGTGATTCGTGCTCTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 GGMTTGTATKCTGCTGCTCTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 146
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTGC 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTGC 206
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 TACTTCTCCGTTACTACTACAGATGACAGGAGCTGCGCCAGTTCCTGTACGAGG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 TACTTCTCCGTTACTACTACAGATGACAGGAGCTGCGCCAGTTCCTGTACGAGG 266
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 GCTGGAAGGGAACGCAACAATTTCTACACCTGGAGGCTTGGACGATGCTTCTGGA 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 267 GCTGGAAGGGAACGCAACAATTTCTACACCTGGAGGCTTGGACGATGCTTCTGGA 326
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGACGACCAATGTGAGG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 327 RGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGACGACCAATGTGAGG 386
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 GGTCCACGAAAAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCG 420
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Db 387 GGTACACAGATTAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCG 446
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 421 GTGGGTGTACCGGAAACCGGATTGAGAACAGTTTCCAGATGAGCTACTGTATGGGCT 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 447 GTGGGTGTACCGGAAACCGGATTGAGAACAGTTTCCAGATGAGCTACTGTATGGGCT 505
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 481 TCTGGCACCAAGAAAAATTCCA 503
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 506 CTTGCRCAACNAAGAAATATATCA 528
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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RESULT 14  
US-09-658-824-64  
;/ Sequence 64, Application US/09658824  
;/ Patent No. 6746846  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Wang, Tongtong  
;/ APPLICANT: Bangur, Chaitanya S.  
;/ APPLICANT: Lodes, Michael A.  
;/ APPLICANT: Fanger, Gary  
;/ APPLICANT: Vedvick, Tom  
;/ APPLICANT: Carter, Darrick  
;/ APPLICANT: Retter, Marc  
;/ APPLICANT: Mannion, Jane  
;/ APPLICANT: Fan, Liqun  
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
;/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
;/ FILE REFERENCE: 210121.478C11  
;/ CURRENT APPLICATION NUMBER: US/09/658,824

;/ CURRENT APPLICATION NUMBER: 2000-09-08  
;/ CURRENT FILING DATE: 2000-09-08  
;/ NUMBER OF SEQ ID NOS: 1788  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 64  
;/ LENGTH: 528  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapien  
;/ FEATURE:  
;/ NAME/KEY: misc.feature  
;/ LOCATION: (1)...(528)  
;/ OTHER INFORMATION: n = A,T,C or G  
US-09-658-824-64

Query Match 45.7%; Score 447; DB 3; Length 528;  
Best Local Similarity 87.5%; Pred. No. 2.7e-115;  
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;

```
QY 1 GGAAGCCCTTGGCCAGCGGCGCCGACCCCTGCAACATGACCCCGCTGCGCCCTGG 60
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Db 27 SGACGCCCTTGGCCAGCGGCGCCGACCCCTGSRCAATGACCCCGCTGCGCCCTGG 86
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GGCTGTGATTCGTGCTCTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 GGMTTGTATKCTGCTGCTCTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 146
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTGC 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 CAACAGAAATTAACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTTGC 206
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 TACTTCTCCGTTACTACTACAGATGACAGGAGCTGCGCCAGTTCCTGTACGAGG 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 207 TACTTCTCCGTTACTACTACAGATGACAGGAGCTGCGCCAGTTCCTGTACGAGG 266
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 GCTGGAAGGGAACGCAACAATTTCTACACCTGGAGGCTTGGACGATGCTTCTGGA 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 267 GCTGGAAGGGAACGCAACAATTTCTACACCTGGAGGCTTGGACGATGCTTCTGGA 326
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QY 301 GGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGACGACCAATGTGAGG 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 327 RGATGAAAAAGTTCCCAAGTTTCCCGCTGCAAGTGTGACGACCAATGTGAGG 386
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 GGTCCACGAAAAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCG 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 387 GGTACACAGATTAAGTATTTCTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCG 446
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 421 GTGGGTGTACCGGAAACCGGATTGAGAACAGTTTCCAGATGAGCTACTGTATGGGCT 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 447 GTGGGTGTACCGGAAACCGGATTGAGAACAGTTTCCAGATGAGCTACTGTATGGGCT 505
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 481 TCTGGCACCAAGAAAAATTCCA 503
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 506 CTTGCRCAACNAAGAAATATATCA 528
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```

RESULT 15  
US-10-017-754-64  
;/ Sequence 64, Application US/10017754  
;/ Patent No. 6858204  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Henderson, Robert A.  
;/ APPLICANT: Wang, Tongtong  
;/ APPLICANT: Watanabe, Yoshihiro  
;/ APPLICANT: Johnson, Jeffrey C.  
;/ APPLICANT: Retter, Marc W.  
;/ APPLICANT: Marnerakis, Margarita  
;/ APPLICANT: Carter, Darrick  
;/ APPLICANT: Fanger, Gary R.  
;/ APPLICANT: Vedvick, Thomas S.  
;/ APPLICANT: Bangur, Chaitanya S.  
;/ APPLICANT: McNabb, Andria  
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;/ FILE REFERENCE: 210121.478C18

/ CURRENT APPLICATION NUMBER: US/10/017,754  
/ CURRENT FILING DATE: 2001-10-29  
/ NUMBER OF SEQ ID NOS: 2004  
/ SOFTWARE: FASTSEQ for Windows Version 4.0  
/ SEQ ID NO 64  
/ LENGTH: 528  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: 374, 443, 444, 452, 476, 489, 515, 523  
/ OTHER INFORMATION: n = A,T,C or G  
US-10-017-754-64

Query Match 45.7%; Score 447; DB 3; Length 528;  
Best Local Similarity 87.5%; Pred. No. 2.7e-115;  
Matches 440; Conservative 42; Mismatches 20; Indels 1; Gaps 1;

QY 1 GGACGCGTTGGCCGAGCGGCGCGCCGAGCCCGCTGACACATGAGACCCCGCTGCGCCCGCTGG 60  
DB 27 SGACGCGCTTGCCGACGCGGCGCGCCGAGCCCGCTGSRCAATGAGACCCCGCTGCGCCGCTGG 86  
QY 61 GAGCTGCGAATTCGTGCTCTTTCTGACGAGAGCTGCACTGGCGATGCTGCTCAGAGC 120  
DB 87 GAGTGTGATKCTGCTGCTTTCTGRCAGAGGCTGCACTGGCGATGCTGATCARAGC 146  
QY 121 CAACGGAATTAACGCGAGATCTGCTCTGCGCCCTAGACTAGGACCTGCGCGGCC 180  
DB 147 CAACGGAATTAACGCGAGATCTGCTCTGCGCCCTAGACTAGGACCTGCGCGGCC 206  
QY 181 TACTTCTCGGTAACACTACGACAGGTACAGGAGCTGCGCGAGTTCTGTACGAGG 240  
DB 207 TACTTTCGATTAACACTACGACAGGTACAGGAGCTGCGCGAGTTCTGTACGAGG 266  
QY 241 GCTGCGAGGCGCAACGCAATTTCTACCTGAGAGCTTGCAGACGATGCTGTGGA 300  
DB 267 GCTGCRASGGCAACGCAATTTCTACACCKGAGGATTCGACATGCTGTGAG 326  
QY 301 GGATGAAAAAGTTCCCAAAGTTGCGGCTGCAAGTAGTGAGACGACAGGTGAG 360  
DB 327 RGATGAAAAAGTTCCCAAAGTTGCGGCTGMAAGTAGAGACGACAGGTGAG 386  
QY 361 GGTCCAGAAAAAGTATTTCTTAATCTAAGTTCAATGACATGTAATAATCTTTCCG 420  
DB 387 GGTACACAGATTAAGTATTTCTTAATCTAATKACCATGACATGTAATAATCTTTNCG 446  
QY 421 GTGGGTGTCACCGAACGATTTGAGAACAGGTTTCAAGTAACTACTTGTATGGCT 480  
DB 447 GTGGGNGTCAACCGG-AACGGAATTGAGAACAGTTTGCAGATGANGCTACTGGGATGGGCT 505  
QY 481 TCTGCGCACCAAGAAAAATTCCA 503  
DB 506 CCTGCRACACNAAAGAAATATCA 528

Search completed: March 11, 2006, 06:08:17  
Job time : 226 secs

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241  GCTGCGAGGGCAACCGCAACAATTTCTACACCTGGAGGGCTTGCAGACGATGCTGCTGGA 300
Qy      301  GGATGAGAAAAGTTGCCAAAGTTTCCGGCTCAGAGTGATGTGACACACGATGTGAGG 360
301  GGATGAGAAAAGTTGCCAAAGTTTCCGGCTCAGAGTGATGTGACACACGATGTGAGG 360
Qy      361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATAGACATGATGAAAATTTCTTTTCG 420
361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATAGACATGATGAAAATTTCTTTTCG 420
Qy      421  GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCAGATGACCTACTTGTATGGCT 480
421  GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCAGATGACCTACTTGTATGGCT 480
Qy      481  TCTGCGCACCAAAAGAAATTCATCATTTTGTCTAAGTCACAAAGATGAGGAGCTGTGCT 540
481  TCTGCGCACCAAAAGAAATTCATCATTTTGTCTAAGTCACAAAGATGAGGAGCTGTGCT 540
Qy      541  CTGCGCAATGTGACTGCTATTTATTTTAATCCAGATPACAGACCTGTATGCTTCACT 600
541  CTGCGCAATGTGACTGCTATTTATTTTAATCCAGATPACAGACCTGTATGCTTCACT 600
Qy      601  ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCGAT 660
601  ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCGAT 660
Qy      661  GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTGCCTTGTGCAATGATCC 720
661  GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTGCCTTGTGCAATGATCC 720
Qy      721  GGAATAATTCGAAAGAGCAATTTTAAATCTTAAATATGCAATGCTTGTGCTTTTNG 780
721  GGAATAATTCGAAAGAGCAATTTTAAATCTTAAATATGCAATGCTTGTGCTTTTNG 780
Qy      781  GCTTATTTGCTTTATGTTGTTGATCTGAAAGATTAATATGACAGATGAGAAACAATCA 840
781  GCTTATTTGCTTTATGTTGTTGATCTGAAAGATTAATATGACAGATGAGAAACAATCA 840
Qy      841  TTGGGATTTATTCACAGATTTTATTAATACAGTCATTTTCAAAAATTTGATTTT 900
841  TTGGGATTTATTCACAGATTTTATTAATACAGTCATTTTCAAAAATTTGATTTT 900
Qy      901  TTTATATTAATTAAGTCTGATTTCAAAATGTAGTCTACATTTTAAATTTATGTTCAAC 960
901  TTTATATTAATTAAGTCTGATTTCAAAATGTAGTCTACATTTTAAATTTATGTTCAAC 960
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961  TGTGAGGAGCTGAATTC 979

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RESULT 2  
US-10-305-720-1378

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; Sequence 1378, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Selhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1378
; LENGTH: 979
; TYPE: DNA

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Genbank ID No. US20040010136A1 9441149
US-10-305-720-1378

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Query Match 100.0%; Score 979, DB 6, Length 979;  
Best Local Similarity 100.0%; Pred. No. 2,8e-247;  
Matches 979, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

Qy      1  GAGGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTG 60
Db      1  GAGGCGCTTGGCCAGCGGGCGCGCCGACCCCTGACACATGAGACCCGCTGCGCCCTG 60
Qy      61  GCGTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTCTCAGAGC 120
61  GCGTGTGATTTCTGTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGTCTCAGAGC 120
Qy      121  CAAACGAAATTAAGCGGAGATCTGTCTCTGCCCCCTTGACTAGAGACCTTGCAGGCCC 180
121  CAAACGAAATTAAGCGGAGATCTGTCTCTGCCCCCTTGACTAGAGACCTTGCAGGCCC 180
Qy      181  TACTTCTCCGTTACTACTACGACAGGTACACGACAGCTGCGCCAGTTCTGTACGGAG 240
181  TACTTCTCCGTTACTACTACTACGACAGGTACACGACAGCTGCGCCAGTTCTGTACGGAG 240
Qy      241  GCTGCGAGGGCAACCGCAACAATTTCTACACTGGAGGCTTGTGCAACGATGCTTGTGGA 300
241  GCTGCGAGGGCAACCGCAACAATTTCTACACTGGAGGCTTGTGCAACGATGCTTGTGGA 300
Qy      301  GGATGAGAAAAGTTCCCAAAGTTTGGCGGCTGCAAGTGAATGTGACACACAGTGTAGG 360
301  GGATGAGAAAAGTTCCCAAAGTTTGGCGGCTGCAAGTGAATGTGACACACAGTGTAGG 360
Qy      361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGATGCAATGAGAAAATTTCTTTTCG 420
361  GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCATGATGCAATGAGAAAATTTCTTTTCG 420
Qy      421  GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCAGATGACCTACTTGTATGGCT 480
421  GTGGGTGTCAACCGGAAACCGGATTTGAGAACAGGTTTCAGATGACCTACTTGTATGGCT 480
Qy      481  TCTGCGCACCAAAAGAAATTCATCATTTTGTCTAAGTCACAAAGATGAGGAGCTGTGCT 540
481  TCTGCGCACCAAAAGAAATTCATCATTTTGTCTAAGTCACAAAGATGAGGAGCTGTGCT 540
Qy      541  CTGCGCAATGTGACTGCTATTTATTTTAATCCAGATPACAGACCTGTATGCTTCACT 600
541  CTGCGCAATGTGACTGCTATTTATTTTAATCCAGATPACAGACCTGTATGCTTCACT 600
Qy      601  ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCGAT 660
601  ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCGAT 660
Qy      661  GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTGCCTTGTGCAATGATCC 720
661  GTGCAAAAGCTTTGAAAAAGAAAGAGAGCCAAAGCTTGCCTTGTGCAATGATCC 720
Qy      721  GGAATAATTCGAAAGAGCAATTTTAAATCTTAAATATGCAATGCTTGTGCTTTTNG 780
721  GGAATAATTCGAAAGAGCAATTTTAAATCTTAAATATGCAATGCTTGTGCTTTTNG 780
Qy      781  GCTTATTTGCTTTATGTTGTTGATCTGAAAGATTAATATGACAGATGAGAAACAATCA 840
781  GCTTATTTGCTTTATGTTGTTGATCTGAAAGATTAATATGACAGATGAGAAACAATCA 840
Qy      841  TTGGGATTTATTCACAGATTTTATTAATACAGTCATTTTCAAAAATTTGATTTT 900
841  TTGGGATTTATTCACAGATTTTATTAATACAGTCATTTTCAAAAATTTGATTTT 900
Qy      901  TTTATATTAATTAAGTCTGATTTCAAAATGTAGTCTACATTTTAAATTTATGTTCAAC 960
901  TTTATATTAATTAAGTCTGATTTCAAAATGTAGTCTACATTTTAAATTTATGTTCAAC 960

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Oy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 3

US-10-680-684-1  
Sequence 1, Application US/10680684  
Publication No. US20040253686A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/10/680,684  
CURRENT FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/09/904,621  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39) ... (746)  
US-10-680-684-1

Query Match 100.0%; Score 979; DB 8; Length 979;

Best Local Similarity 100.0%; Pred. No. 2.8e-247; Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGGACCATGAGACCCCTGCGCCCTGCG 60  
Db 1 GAGAGCCCTTGGCCAGCGGGGCGCCGAGCCCTTGGACCATGAGACCCCTGCGCCCTGCG 60  
Oy 61 GCGTGTGATTCGTGCTCTTTTCTGACGAGGCTGCACTGCGCGATGCTGCTCAGAGC 120  
Db 61 GCGTGTGATTCGTGCTCTTTTCTGACGAGGCTGCACTGCGCGATGCTGCTCAGAGC 120  
Oy 121 CAACGAGAAATACCGCGAGATCTGCTCTCCCTTGAATAAGGACCCCTGCGGGGCC 180  
Db 121 CAACGAGAAATACCGCGAGATCTGCTCTCCCTTGAATAAGGACCCCTGCGGGGCC 180  
Oy 181 TACTTCTCGTTACTATACGACAGGTACAGGAGCTGCGGAGTTCTGTACGGGG 240  
Db 181 TACTTCTCGTTACTATACGACAGGTACAGGAGCTGCGGAGTTCTGTACGGGG 240  
Oy 241 GCTGGAAGGCAACGCAACATTTCTACCTGGAAGCTTGCAGCATGCTTGCCTGA 300  
Db 241 GCTGGAAGGCAACGCAACATTTCTACCTGGAAGCTTGCAGCATGCTTGCCTGA 300  
Oy 301 GGAATGAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAAGCAACAGTGAAG 360  
Db 301 GGAATGAAAAGTTCCCAAGTTTCCGGCTGCAAGTGAAGTGAAGCAACAGTGAAG 360  
Oy 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCCATGACATGTAATAAATTTCTTTCCG 420  
Db 361 GGTCCACAGAAAAGTATTTCTTAATCTAAGTTCCATGACATGTAATAAATTTCTTTCCG 420  
Oy 421 GTGGGTGTCACCGAAGCGGATGAGAACAGGTTTCAAGTAAAGCTATCTGTATGGCT 480  
Db 421 GTGGGTGTCACCGAAGCGGATGAGAACAGGTTTCAAGTAAAGCTATCTGTATGGCT 480

Oy 481 TCTGCGACCAAGAAAATTCATCATTTTGTCTACAGTCGCAAGAGAGAGAGCTGCT 540  
Db 481 TCTGCGACCAAGAAAATTCATCATTTTGTCTACAGTCGCAAGAGAGAGAGCTGCT 540  
Oy 541 CTGCGAATGTGACTCGCTATTATTTTAATCCAGATACAGAACTGTGATCTTCACT 600  
Db 541 CTGCGAATGTGACTCGCTATTATTTTAATCCAGATACAGAACTGTGATCTTCACT 600  
Oy 601 ATACTGCTGTGAGGAGAAATGACATTAATTTGTAGAGGAGAGATTGCAAGTGCAT 660  
Db 601 ATACTGCTGTGAGGAGAAATGACATTAATTTGTAGAGGAGAGATTGCAAGTGCAT 660  
Oy 661 GTGCAAAAAGCTTTGAAAAGAAAAGAGATGCCAAAGCTTGCCTTGCAGTAGATCC 720  
Db 661 GTGCAAAAAGCTTTGAAAAGAAAAGAGATGCCAAAGCTTGCCTTGCAGTAGATCC 720  
Oy 721 GGAATAATCGAAGAGCAATTTTAAACATTTTAATATGTCATCTTGTGCTTTATG 780  
Db 721 GGAATAATCGAAGAGCAATTTTAAACATTTTAATATGTCATCTTGTGCTTTATG 780  
Oy 781 GCTTATTTGCTTTATGTTGTATCTGAGAAATATATGACATGAGAAACAAATCA 840  
Db 781 GCTTATTTGCTTTATGTTGTATCTGAGAAATATATGACATGAGAAACAAATCA 840  
Oy 841 TTGGGATTTATTCACAGTTTATTTATTAATCAAGTCACTTTTCAAAAATTTGATTT 900  
Db 841 TTGGGATTTATTCACAGTTTATTTATTAATCAAGTCACTTTTCAAAAATTTGATTT 900  
Oy 901 TTTATATTAATCAAGTCTAATTCAAATGAGTCTACATTTTAAATTTATGTTCAAC 960  
Db 901 TTTATATTAATCAAGTCTAATTCAAATGAGTCTAATTTTAAATTTATGTTCAAC 960  
Oy 961 TGTGTGAGACTGAATTC 979  
Db 961 TGTGTGAGACTGAATTC 979

## RESULT 4

US-10-800-057-1  
Sequence 1, Application US/10800057

Publication No. US2005004021A1  
GENERAL INFORMATION:  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Kiesel, Walter  
APPLICANT: Foster, Donald C.  
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS  
TITLE OF INVENTION: AND  
FILE REFERENCE: 93-14D3  
CURRENT APPLICATION NUMBER: US/10/800,057  
CURRENT FILING DATE: 2004-03-12  
PRIOR APPLICATION NUMBER: US/10/680,684  
PRIOR FILING DATE: 2003-10-07  
PRIOR APPLICATION NUMBER: US/09/904,621  
PRIOR FILING DATE: 2001-07-13  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 09/265,627  
PRIOR FILING DATE: PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 5,455,338  
PRIOR FILING DATE: PRIOR FILING DATE: 1993-11-05  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 979  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (39) ... (746)  
US-10-800-057-1

Query Match 100.0%; Score 979; DB 8; Length 979;  
Best Local Similarity 100.0%; Pred. No. 2.8e-247; Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGCCAGAGGCGGCGGAGCCCTCTGACCAATGAGACCCCGCTGCGCCCTGG 60  
DB 1 GGAAGCCTTGCCAGAGGCGGCGGAGCCCTCTGACCAATGAGACCCCGCTGCGCCCTGG 60  
QY 61 GAGCTGCAATTCGTGCGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
DB 61 GAGCTGCAATTCGTGCGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
QY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCCCTGCGGCGC 180  
DB 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCCCTGCGGCGC 180  
QY 181 TACTTCTCCGTTACTACTACAGAGGTACAGCAGAGCTGCGCACTTCTGTACGAGG 240  
DB 181 TACTTCTCCGTTACTACTACAGAGGTACAGCAGAGCTGCGCACTTCTGTACGAGG 240  
QY 241 GCTGAGAGGCGCAACGCAATTTCTACACTGGGAGGCTTGGACAGATGCTGTCTGGA 300  
DB 241 GCTGAGAGGCGCAACGCAATTTCTACACTGGGAGGCTTGGACAGATGCTGTCTGGA 300  
QY 301 GGAATGAAAAAGTCCCAAGTTTGGCGGCTGCAAGTGAAGTGAAGCACTGTGAGG 360  
DB 301 GGAATGAAAAAGTCCCAAGTTTGGCGGCTGCAAGTGAAGTGAAGCACTGTGAGG 360  
QY 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCCG 420  
DB 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCCG 420  
QY 421 GTGGGATGCAACGGAACGGAATTTGAACAAGTTCCAGATGAGCTCTGTATGGGCT 480  
DB 421 GTGGGATGCAACGGAACGGAATTTGAACAAGTTCCAGATGAGCTCTGTATGGGCT 480  
QY 481 TCTGCGCACCAAAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 481 TCTGCGCACCAAAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
QY 541 CTGCGCAATGTGACTGCGCTAATTTTAAATCCAAATACAGAACTGTGATGCTTCACTT 600  
DB 541 CTGCGCAATGTGACTGCGCTAATTTTAAATCCAAATACAGAACTGTGATGCTTCACTT 600  
QY 601 ATACTGCGCTGAGGAGGAGTGAACAATACTTTGAGCAGGAGGATTTGCAAAAGCTGAT 660  
DB 601 ATACTGCGCTGAGGAGGAGTGAACAATACTTTGAGCAGGAGGATTTGCAAAAGCTGAT 660  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGGCTTCCAGTAGAATCC 720  
DB 661 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGGCTTCCAGTAGAATCC 720  
QY 721 GGAATAATCGAAGAGCAATTTAAACATTTCTTAATATGTCATCTTGTGTCTTTATG 780  
DB 721 GGAATAATCGAAGAGCAATTTAAACATTTCTTAATATGTCATCTTGTGTCTTTATG 780  
QY 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGCTGAGAAACAAATCA 840  
DB 781 GCTTATTTGCTTTATGTTGTTATCTGAAGATTAATATGACAGCTGAGAAACAAATCA 840  
QY 841 TTGAGTATTTATCCAGATTTTAAATATGACAGCTTCTTCAAAAATTTGAGATTT 900  
DB 841 TTGAGTATTTATCCAGATTTTAAATATGACAGCTTCTTCAAAAATTTGAGATTT 900  
QY 901 TTTATATATTAAGTCTGCTAATTTCAATGTGAGTCTACATTTTAAATTTATGTTCAAC 960  
DB 901 TTTATATATTAAGTCTGCTAATTTCAATGTGAGTCTACATTTTAAATTTATGTTCAAC 960  
QY 961 TGTGTTGAGACTGAATTC 979  
DB 961 TGTGTTGAGACTGAATTC 979

RESULT 5  
US-10-060-036-145  
; Sequence 145, Application US/10060036

; Publication No. US20030073144A1  
; GENERAL INFORMATION:  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Persing, David H.  
; APPLICANT: Hepler, William T.  
; APPLICANT: Jiang, Yugu  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 145  
; LENGTH: 1172  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-060-036-145

Query Match 100.0%; Score 979; DB 5; Length 1172;  
Best Local Similarity 100.0%; Pred. No. 3.1e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGCCTTGCCAGAGGCGGCGGAGCCCTCTGACCAATGAGACCCCGCTGCGCCCTGG 60  
DB 38 GGAAGCCTTGCCAGAGGCGGCGGAGCCCTCTGACCAATGAGACCCCGCTGCGCCCTGG 97  
QY 61 GAGCTGCAATTCGTGCGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAGC 120  
DB 98 GAGCTGCAATTCGTGCGCTTTCTGAGGAGGCTGCACTGGGCGATGCTGCTCAGAGAGC 157  
QY 121 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCCCTGCGGCGC 180  
DB 158 CAACAGAAATTAACGCGAGATCTGTCTCTGCGCCCTAGACTACGAGACCCCTGCGGCGC 217  
QY 181 TACTTCTCCGTTACTACTACAGAGGTACAGCAGAGCTGCGCACTTCTGTACGAGG 240  
DB 218 TACTTCTCCGTTACTACTACAGAGGTACAGCAGAGCTGCGCACTTCTGTACGAGG 277  
QY 241 GCTGAGAGGCGCAACGCAATTTCTAACAATGAGGAGGCTTGGACAGATGCTGTCTGGA 300  
DB 278 GCTGAGAGGCGCAACGCAATTTCTAACAATGAGGAGGCTTGGACAGATGCTGTCTGGA 337  
QY 301 GGAATGAAAAAGTCCCAAGTTTGGCGGCTGCAAGTGAAGTGAAGCACTGTGAGG 360  
DB 338 GGAATGAAAAAGTCCCAAGTTTGGCGGCTGCAAGTGAAGTGAAGCACTGTGAGG 397  
QY 361 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCCG 420  
DB 398 GGTCCACAGAAAAATTTCTTTAATCTAAGTTCCATGACATGTGAAAAATTTCTTTCCG 457  
QY 421 GTGGGATGCAACGGAACGGAATTTGAACAAGTTTCCAGATGAGCTCTGTATGGGCT 480  
DB 458 GTGGGATGCAACGGAACGGAATTTGAACAAGTTTCCAGATGAGCTCTGTATGGGCT 517  
QY 481 TCTGCGCACCAAAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
DB 518 TCTGCGCACCAAAAGAAATTCATCTTTGCTACAGTCCAAAGATGAGGAGCTGTGCT 577  
QY 541 CTGCGCAATGTGACTGCGCTAATTTTAAATCCAAATATGACAGCTGTGATGCTTCACTT 600  
DB 578 CTGCGCAATGTGACTGCGCTAATTTTAAATCCAAATATGACAGCTGTGATGCTTCACTT 637  
QY 601 ATACTGCTGAGGAGGAGTGAACAATACTTTGTTAAGAGGAGATTTGCAAAAGTGTAT 660  
DB 638 ATACTGCTGAGGAGGAGTGAACAATACTTTGTTAAGAGGAGATTTGCAAAAGTGTAT 697  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGGCTTCCAGTAGAATCC 720  
DB 698 GTGCAAAAGCTTTGAAAAAGAAAGATCCAAAGCTTGGCTTCCAGTAGAATCC 757



Query Match 100.0%; Score 979; DB 3; Length 2407;  
Best Local Similarity 100.0%; Pred. No. 4,7e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCAGCGGGCGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTCG 60  
74 GAGCCCTTGGCCAGCGGGCGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTCG 133  
61 GAGCTGCAATCTGCTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTGACAGAGC 120  
134 GAGCTGCAATCTGCTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTGACAGAGC 193  
121 CAACGGAATTAACCGGAGATCTGCTGCTGCGCCCTGAGACTAGCGAACCTGCGCGGCC 180  
194 CAACGGAATTAACCGGAGATCTGCTGCTGCGCCCTGAGACTAGCGAACCTGCGCGGCC 253  
181 TACTCTCGTTACTACTACGACAGGTACAGGACGCGCGCATGCTGCTGACGAGG 240  
254 TACTCTCGTTACTACTACGACAGGTACAGGACGCGCGCATGCTGCTGACGAGG 313  
241 GCTGCGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGACGATGCTGCTGGA 300  
314 GCTGCGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGACGATGCTGCTGGA 373  
301 GGATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACAAGTGAAG 360  
374 GGATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACAAGTGAAG 433  
351 GGTCACAGAAAAAGTATTTCTTAATCTAAGTTCAGATGCAATGAAAAATTTCTTTCCG 420  
434 GGTCCACAGAAAAAGTATTTCTTAATCTAAGTTCAGATGCAATGAAAAATTTCTTTCCG 493  
421 GTGGGTGTACCGGACCGGATGGAACAAGTTTCCAGATGAACTACTGTATGAGCT 480  
494 GTGGGTGTACCGGACCGGATGGAACAAGTTTCCAGATGAACTACTGTATGAGCT 553  
481 TCTGGGCAACCAAGAAAAATTCATCAATTTGCTACAGTCCAAAGATGAGGAGCTGTCT 540  
554 TCTGGGCAACCAAGAAAAATTCATCAATTTGCTACAGTCCAAAGATGAGGAGCTGTCT 613  
541 CTGGCAATGTGACTGCTATTAATTTTAATCCAGATGAGAACCTGTATGCTTCACT 600  
614 CTGGCAATGTGACTGCTATTAATTTTAATCCAGATGAGAACCTGTATGCTTCACT 673  
601 ATACTGCTGTGAGGAGATGACATTAATTTGTTAGCAGGAGGATGCAACCTGAT 660  
674 ATACTGCTGTGAGGAGATGACATTAATTTGTTAGCAGGAGGATGCAACCTGAT 733  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTCCAGTGAATCC 720  
734 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTCCAGTGAATCC 793  
721 GGAATAATCGAAGAAAGATTTTAAACATTTTAATATGTCATGTTGTGCTTAAG 780  
794 GGAATAATCGAAGAAAGATTTTAAACATTTTAATATGTCATGTTGTGCTTAAG 853  
781 GCTTATTTGCTTATGTTGATCTGAAGATATATATGACAGATGAGAAACATATCA 840  
854 GCTTATTTGCTTATGTTGATCTGAAGATATATATGACAGATGAGAAACATATCA 913  
841 TTGGTATTTATTCACAGGTTTATTAATACAGTCACTTTTCAAAAAATTTGATTTT 900  
914 TTGGTATTTATTCACAGGTTTATTAATACAGTCACTTTTCAAAAAATTTGATTTT 973  
901 TTTATATTAATCTAGCTGCTATTCAAAGTGAAGTACATTTTAATTTAATGTTGAC 960  
974 TTTATATTAATCTAGCTGCTATTCAAAGTGAAGTACATTTTAATTTAATGTTGAC 1033  
961 TGTGTTGAGACTGAATTC 979  
1034 TGTGTTGAGACTGAATTC 1052

RESULT 8  
US-10-044-090-609  
; Sequence 609, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Olga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044, 090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 609  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 181172CB1  
US-10-044-090-609

Query Match 100.0%; Score 979; DB 5; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 4,8e-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAAGCCCTTGGCCAGCGGGCGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTCG 60  
27 GAGCCCTTGGCCAGCGGGCGCGCCGACCCCTGACCATGAGACCCCGCTGCGCCCTCG 86  
61 GAGCTGCAATCTGCTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTGACAGAGC 120  
87 GAGCTGCAATCTGCTGCTTTTCTGACGAGAGCTGCACTGGCGCATGCTGCTGACAGAGC 146  
121 CAACGGAATTAACCGGAGATCTGCTGCTGCGCCCTGAGACTAGCGAACCTGCGCGGCC 180  
147 CAACGGAATTAACCGGAGATCTGCTGCTGCGCCCTGAGACTAGCGAACCTGCGCGGCC 206  
181 TACTTCTCGTTACTACTACGACAGGTACAGGACGCGCGCATGCTGCTGACGAGG 240  
207 TACTTCTCGTTACTACTACGACAGGTACAGGACGCGCGCATGCTGCTGACGAGG 266  
241 GCTGCGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGAGAGATGCTTGTGGA 300  
267 GCTGCGAGGCGCAACCGCAATTTCTACACCTGGAGGCTTGGAGAGATGCTTGTGGA 326  
301 GGATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACAAGTGAAG 360  
327 GGATGAAAAAGTTCCCAAGTTTCCGCTGCAAGTGAAGTGAAGCAACAAGTGAAG 386  
361 GGTCCACAGAAAAATGATTTCTTAATCTAAGTTCATGACATGTGAATAATTTCTTTCCG 420  
387 GGTCCACAGAAAAATGATTTCTTAATCTAAGTTCATGACATGTGAATAATTTCTTTCCG 446  
421 GTGGGTGTACCGGACCGGATGGAACAAGTTTCCAGATGAACTACTGTATGAGCT 480  
447 GTGGGTGTACCGGACCGGATGGAACAAGTTTCCAGATGAACTACTGTATGAGCT 506  
481 TCTGCGACCAAGAAAAATTCATGTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 540  
507 TCTGCGACCAAGAAAAATTCATGTTTGTCTACAGTCCAAAGATGAGGAGCTGTGCT 566  
541 CTGGCAATGTGACTGCTATTAATTTTAATCCAGATGAGAACCTGTATGCTTCACT 600  
567 CTGGCAATGTGACTGCTATTAATTTTAATCCAGATGAGAACCTGTATGCTTCACT 626  
601 ATACTGCTGTGAGGAGATGACATTAATTTGTTAGCAGGAGAGATTTGCAACGTGAT 660  
627 ATACTGCTGTGAGGAGATGACATTAATTTGTTAGCAGGAGAGATTTGCAACGTGAT 686  
661 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTCCAGTGAATCC 720  
687 GTGCAAAAGCTTTGAAAAAGAAAGATGCGCAAGCTTGGCTTCCAGTGAATCC 746

Qy 721 GGAATTCGGAAGAGCAATTTAAGATCTTAATATGATCTGTTGCTTTTANG 780  
Db 747 GGAATTCGGAAGAGCAATTTAAGATCTTAATATGATCTGTTGCTTTTANG 806  
Qy 781 GCTATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 807 GCTATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866  
Qy 841 TTGGGATTTATTCACCGCTTTTATTTATTTATTTATTTATTTATTTATTTATTT 900  
Db 867 TTGGGATTTATTCACCGCTTTTATTTATTTATTTATTTATTTATTTATTTATTT 926  
Qy 901 TTATATATATATCTAGCTGATTTCAATGATGATGATGATGATGATGATGATGATGAT 960  
Db 927 TTATATATATATCTAGCTGATTTCAATGATGATGATGATGATGATGATGATGATGAT 986  
Qy 961 TGTTCGAGACTGAATTC 979  
Db 987 TGTTCGAGACTGAATTC 1005

RESULT 9  
US-10-084-817-143  
Sequence 143, Application US/10084817  
Publication No. US20030119009A1  
GENERAL INFORMATION:  
APPLICANT: Susan Stuart  
APPLICANT: Jed G. Nuchtern  
APPLICANT: Sharon E. Plon  
APPLICANT: Jason M. Shohet  
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION  
FILE REFERENCE: PA-0046 US  
CURRENT APPLICATION NUMBER: US/10/084,817  
CURRENT FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: 60/270,784  
PRIOR FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 365  
SOFTWARE: PERL Program  
SEQ ID NO 143  
LENGTH: 2540  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. US20030119009A1 181172CBI  
US-10-084-817-143

Query Match 100.0%; Score 979; DB 5; Length 2540;  
Best Local Similarity 100.0%; Pred. No. 4,88-247;  
Matches 979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACATGAGCCCGCTGCGCCCTGG 60  
Db 27 GGAAGCGCTTGGCCAGCGGCGCGCCGACCCCTGACATGAGCCCGCTGCGCCCTGG 86  
Qy 61 GCGTGTGATTTCTGCTCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAC 120  
Db 87 GCGTGTGATTTCTGCTCTTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTGAGAC 146  
Qy 121 CAACAGAAATTAAGCGGAGATCTGCTCTGACGAGAGCGGAGCGGAGCGGAGCGG 180  
Db 147 CAACAGAAATTAAGCGGAGATCTGCTCTGACGAGAGCGGAGCGGAGCGGAGCGG 206  
Qy 181 TACTTCTCGTTACTACTACGACGATACGACGACGATGCGGACGATTCCTGTAAGGAG 240  
Db 207 TACTTCTCGTTACTACTACGACGATACGACGACGATGCGGACGATTCCTGTAAGGAG 266  
Qy 241 GCTGGAAGGCAAGCGCAATTTCTTACACTGGAAGGCTTGGCAAGATGCTTCTGGA 300  
Db 267 GCTGGAAGGCAAGCGCAATTTCTTACACTGGAAGGCTTGGCAAGATGCTTCTGGA 326  
Qy 301 GGATGAAAAAGTTGCCAAAGTTGCCGAGCTGCAAGTAGTGTGACGACGAGTGTGAGG 360

Db 327 GGATGAAAAAGTTGCCAAAGTTGCCGAGCTGCAAGTAGTGTGACGACGAGTGTGAGG 386  
Qy 361 GGTCCACGAAAGATTTCTTTATATCTAAGTCCATGACATGTGAAATTTCTTTCCG 420  
Db 387 GGTCCACGAAAGATTTCTTTATATCTAAGTCCATGACATGTGAAATTTCTTTCCG 446  
Qy 421 GTGGGTGACCGGAAACCGGATGAGACAGATTTCCAGATGAGCTACTGTATGAGGCT 480  
Db 447 GTGGGTGACCGGAAACCGGATGAGACAGATTTCCAGATGAGCTACTGTATGAGGCT 506  
Qy 481 TCTGGCACCAAGAAATTCATCTTTTCTACGTCAGTCCAAAGATGAGGAGCTGTGCT 540  
Db 507 TCTGGCACCAAGAAATTCATCTTTTCTACGTCAGTCCAAAGATGAGGAGCTGTGCT 566  
Qy 541 CTGCCAATGTGACTGCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 600  
Db 567 CTGCCAATGTGACTGCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 626  
Qy 601 ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCAT 660  
Db 627 ATACTGCTGTGAGGAGGATGACAAATTAATTTGTTAGCAGGAGGATTTGCAACGTCAT 686  
Qy 661 GTGCAAAAGCTTTGAAAAAGAAAAAGATGCCAAGCTTGCCTTSCAGTAGAATCC 720  
Db 687 GTGCAAAAGCTTTGAAAAAGAAAAAGATGCCAAGCTTGCCTTSCAGTAGAATCC 746  
Qy 721 GGAATTCGGAAGAGCAATTTAAGATCTTAATATGATCTGTTGCTTTTANG 780  
Db 747 GGAATTCGGAAGAGCAATTTAAGATCTTAATATGATCTGTTGCTTTTANG 806  
Qy 781 GCTATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840  
Db 807 GCTATTCCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 866  
Qy 841 TTGGGATTTATTCACCGCTTTTATTTATTTATTTATTTATTTATTTATTTATTT 900  
Db 867 TTGGGATTTATTCACCGCTTTTATTTATTTATTTATTTATTTATTTATTTATTT 926  
Qy 901 TTATATATATATCTAGCTGATTTCAATGATGATGATGATGATGATGATGATGATGAT 960  
Db 927 TTATATATATATCTAGCTGATTTCAATGATGATGATGATGATGATGATGATGATGAT 986  
Qy 961 TGTTCGAGACTGAATTC 979  
Db 987 TGTTCGAGACTGAATTC 1005

RESULT 10  
US-10-097-340-315  
Sequence 315, Application US/10097340  
Publication No. US20030087250A1  
GENERAL INFORMATION:  
APPLICANT: John MONAHAN  
APPLICANT: Manjula GANNABARAPU  
APPLICANT: Sebastian HOBBSCH  
APPLICANT: Shudhangli KAMATKAR  
APPLICANT: Steve G. KOVATS  
APPLICANT: Rachel E. MEYERS  
APPLICANT: Michael MORRISSEY  
APPLICANT: Peter OLANDT  
APPLICANT: Ami SEN  
APPLICANT: Peter VEIBY  
APPLICANT: Gordon B. MILLS  
APPLICANT: Robert C. BAST, Jr.  
APPLICANT: Karen LU  
APPLICANT: Rosemarie SCHMANDT  
APPLICANT: Xumei ZHAO  
APPLICANT: Karen GLATT  
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
FILE REFERENCE: MRI-030  
CURRENT APPLICATION NUMBER: US/10/097,340



```

; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 315
; LENGTH: 1142
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-315

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Query Match 99.3%; Score 972.2; DB 5; Length 1142;

Best Local Similarity 99.7%; Pred. No. 1.9e-245;

Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GGAGCCCTTGGCCAGCGGCGCGCCGAGCCCTGACACATGAGACCCGCTGCGCCCTG 60
DB 19 GGAAGCCCTTGGCCAGCGGCGCGCGCCGAGCCCTGACACATGAGACCCGCTGCGCCCTG 78
QY 61 GGCTGTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
DB 79 GGCTGTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 138
QY 121 CAACGAGAAATPACCGGAGATCTCTCCCTGACATGAGACCCCTGCGGCGCC 180
DB 139 CAACGAGAAATPACCGGAGATCTCTCTCCCTGACATGAGACCCCTGCGGCGCC 198
QY 181 TACTTCTCCGTTACTACTACGACAGATACAGCAGAGCTGCGGCGATTTCTGACGAGG 240
DB 199 TACTTCTCCGTTACTACTACGACAGATACAGCAGAGCTGCGGCGATTTCTGACGAGG 258
QY 241 GCTGCGAGGCGCAAGCCCAATTTCTACACTGAGGAGCTTGCAGACATGCTTGCAG 300
DB 259 GCTGCGAGGCGCAAGCCCAATTTCTACACTGAGGAGCTTGCAGACATGCTTGCAG 318
QY 301 GGATGAGAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAACAAGTGTGAGG 360
DB 319 GGATGAGAAAGTTCCCAAGTTTCCGCGCTGCAAGTGAAGTGAACAAGTGTGAGG 378
QY 361 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 420
DB 379 GGTCCACAGAAAGTATTTCTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 438
QY 421 GTGGGTGTCACCGGAAACCGAATGAGAACAGGTTTCCAGATGAAGCTATCTGTATG 480
DB 439 GTGGGTGTCACCGGAAACCGAATGAGAACAGGTTTCCAGATGAAGCTATCTGTATG 498
QY 481 TCTGGGCAACAAAGAAATTCATCAATTTGCTAAGTCCAAAGTAAGAGGAGCTGTGCT 540
DB 499 TCTGGGCAACAAAGAAATTCATCAATTTGCTAAGTCCAAAGTAAGAGGAGCTGTGCT 558
QY 541 CTGCAATGTGATCTGCTATTTAATTTAATCCAAAGTACAGAACTGTATGCTTCACT 600
DB 559 CTGCAATGTGATCTGCTATTTAATTTAATCCAAAGTACAGAACTGTATGCTTCACT 618
QY 601 AATCTGCTGTGAGAGGAAATGCAATTAATTTGTTAGAGAGGAGATTCAGAACTGTAT 660
DB 619 AATCTGCTGTGAGAGGAAATGCAATTAATTTGTTAGAGAGGAGATTCAGAACTGTAT 678
QY 661 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTCCCTTTCCTGATGAATCC 720

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DB 679 GTGCAAAAGCTTTGAAAGAAAGAAAGATGCCAAAGCTTCCCTTTCCTGATGAATCC 738
QY 721 GAAATATCGAAGAGCAATTTTAAATTTAATATGATCATCTTTGCTTTTANG 780
DB 739 GAAATATCGAAGAGCAATTTTAAATTTAATATGATCATCTTTGCTTTTANG 798
QY 781 GCTTATTTGCTTATGTTGTATCTGAAGATATATATGACAGATGAGAAACAAATCA 840
DB 799 GCTTATTTGCTTATGTTGTATCTGAAGATATATATGACAGATGAGAAACAAATCA 858
QY 841 TTGGATTTATATACCAAGTTTATTTAATTAATCAAGTCACTTTCAAAAATTTGATTTT 900
DB 859 TTGGATTTATATCAAGTTTATTTAATTAATCAAGTCACTTTCAAAAATTTGATTTT 918
QY 901 TTTATATTAATTAAGTCTGCTATTTCAATATGATGCTACATTTTATTAATTAATGTTCAAC 960
DB 919 TTTATATTAATTAAGTCTGCTATTTCAATATGATGCTACATTTTATTAATTAATGTTCAAC 978
QY 961 TGTTTGTGAGACTGAAT 977
DB 979 TGTTTGTGAGACTGAAT 995

```

RESULT 11

US-10-021-660-53

; Sequence 53, Application US/10021660

; Publication No. US20030152926a1

; GENERAL INFORMATION:

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: EOS Biotechnology, Inc.

; TITLE OF INVENTION: No. US20030152926a1e1 Methods of Diagnosis of Angiogenesis,

; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis

; FILE REFERENCE: 018501-000710US

; CURRENT APPLICATION NUMBER: US/10/021,660

; PRIOR FILING DATE: 2001-12-06

; PRIOR FILING DATE: 2001-02-14

; PRIOR FILING DATE: 2000-08-11

; NUMBER OF SEQ ID NOS: 135

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 53

; LENGTH: 1142

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-021-660-53

Query Match 99.3%; Score 972.2; DB 6; Length 1142;

Best Local Similarity 99.7%; Pred. No. 1.9e-245;

Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GGAGCCCTTGGCCAGCGGCGCGCCGAGCCCTGACACATGAGACCCGCTGCGCCCTG 60
DB 19 GGAAGCCCTTGGCCAGCGGCGCGCGCCGAGCCCTGACACATGAGACCCGCTGCGCCCTG 78
QY 61 GGCTGTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 120
DB 79 GGCTGTGATTTGCTGCTTTTCTGACGAGGCTGCACTGGGCGATGCTGCTCAGAGC 138
QY 121 CAACGAGAAATPACCGGAGATCTGTCTCTGACCCTAGACTAGAGACCTGCGGCGCC 180
DB 139 CAACGAGAAATPACCGGAGATCTGTCTCTGACCCTAGACTAGAGACCTGCGGCGCC 198
QY 181 TACTTCTCCGTTACTACTACGACAGATACAGCAGAGCTGCGGCGATTTCTGACGAGG 240
DB 199 TACTTCTCCGTTACTACTACGACAGATACAGCAGAGCTGCGGCGATTTCTGACGAGG 258
QY 241 GCTGCGAGGCGCAAGCCCAATTTCTACACTGAGGAGCTTGCAGACATGCTTGCAG 300
DB 259 GCTGCGAGGCGCAAGCCCAATTTCTACACTGAGGAGCTTGCAGACATGCTTGCAG 318

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QY 661 GTGCAAAAGCTTTGAAAAAGAAAAGAGATCCAAAGCTTGGCTTTGCAAGATGATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAGATCCAAAGCTTGGCTTTGCAAGATGATCC 738  
QY 721 GGAATAATTCGAAAGAGCAATTTTAACTTTCTTAATATGTATCTTTGTTGCTTTATG 780  
DB 739 GGAATAATTCGAAAGAGCAATTTTAACTTTCTTAATATGTATCTTTGTTGCTTTATG 798  
QY 781 GCTTAATTCGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
DB 799 GCTTAATTCGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGATGATTTATTCACAGATTTTAACTTAATCAAGTCACTTTTCAAAAATTTGATTTT 900  
DB 859 TTGATGATTTATTCACAGATTTTAACTTAATCAAGTCACTTTTCAAAAATTTGATTTT 918  
QY 901 TTTAATATTAATTAAGTCTGATATTCAAATGATGCTACATTTTAAATTTATGTTCAAC 960  
DB 919 TTTAATATTAATTAAGTCTGATATTCAAATGATGCTACATTTTAAATTTATGTTCAAC 978  
QY 961 TGTGTTGAGACTGAAT 977  
DB 979 TGTGTTGAGACTGAAT 995

RESULT 13  
US-10-428-487-6

; Sequence 6, Application US/10428487  
; Publication No. US20040006780A1  
; GENERAL INFORMATION:  
; APPLICANT: RASTELLI, LUCA K.  
; APPLICANT: GERBER, HANS-PETER  
; TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM  
; FILE REFERENCE: 09800080-0103  
; CURRENT APPLICATION NUMBER: US/10/428,487  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: 09/815,153  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,201  
; PRIOR FILING DATE: 2000-03-22  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1142  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-428-487-6

Query Match 99.3%; Score 972.2; DB 6; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGAAGCCCTTGGCCAGAGCGGCGCCGAGCCCTCTGACACATGAGACCCCGCTGCCCCCTGG 60  
DB 19 GAGCCCTTGGCCAGAGCGGCGCCGAGCCCTCTGACACATGAGACCCCGCTGCCCCCTGG 78  
QY 61 GAGTGTCAATTCGTGCTTTTCTGAGAGAGCTGCACTGGGCGATGCTGCTCAGAGAC 120  
DB 79 GAGTGTCAATTCGTGCTTTTCTGAGAGAGCTGCACTGGGCGATGCTGCTCAGAGAC 138  
QY 121 CAACAGAAATPACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 180  
DB 139 CAACAGAAATPACGCGAGATCTGTCTCTGCCCCCTAGACTACGAGACCTGCGGAGCC 198  
QY 181 TACTTCTCCGTTACTACATACAGAGTACAGCAGACGTCGCCGCCAGTTCTCTGACGGGG 240  
DB 199 TACTTCTCCGTTACTACATACAGAGTACAGCAGACGTCGCCGCCAGTTCTCTGACGGGG 258  
QY 241 GCTGGAAGGCAAGCCAAATTTCTACACTTGGAGAGCTTGGACAGATGCTGCTGGA 300  
DB 259 GCTGGAAGGCAAGCCAAATTTCTACACTTGGAGAGCTTGGACAGATGCTGCTGGA 318

QY 301 GGAATGAAAAAGTTCCCAAGCTTGGCCGCTGCAAGTATGTGAGCAAGTGTGAG 360  
DB 319 GGAATGAAAAAGTTCCCAAGCTTGGCCGCTGCAAGTATGTGAGCAAGTGTGAG 378  
QY 361 GGTCCAGAAAAATGATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 420  
DB 379 GGTCCAGAAAAATGATTTCTTTAATCTAAGTTCATGACATGTGAAAAATTTCTTTCCG 438  
QY 421 GTGGGTGTCACCGGAACCGGATGAGAACAGTTTCCAGATGAAGCTACTTGTATGGCT 480  
DB 439 GTGGGTGTCACCGGAACCGGATGAGAACAGTTTCCAGATGAAGCTACTTGTATGGCT 498  
QY 481 TCTGGGCAAGAAAAATTCATCTTTTCTACAGTCCAAAGATGAGGAGCTGCT 540  
DB 499 TCTGGGCAAGAAAAATTCATCTTTTCTACAGTCCAAAGATGAGGAGCTGCT 558  
QY 541 CTGCAATGTGACCTGCTAATTTTAACTCAAGATACAGAACTGTGATGCTTCACT 600  
DB 559 CTGCAATGTGACCTGCTAATTTTAACTCAAGATACAGAACTGTGATGCTTCACT 618  
QY 601 ATACTGCTGTGAGAGGAATGACATTAATTTTGAAGGAGGATGCAAAAGCTGAT 660  
DB 619 ATACTGCTGTGAGAGGAATGACATTAATTTTGAAGGAGGATGCAAAAGCTGAT 678  
QY 661 GTGCAAAAGCTTTGAAAAAGAAAAGATGCCAAAGCTTGGCCAGTGAATCC 720  
DB 679 GTGCAAAAGCTTTGAAAAAGAAAAGATGCCAAAGCTTGGCCAGTGAATCC 738  
QY 721 GGAATAATTCGAAAGAGCAATTTTAACTTTCTTAATATGTATCTTTGTTGCTTTATG 780  
DB 739 GGAATAATTCGAAAGAGCAATTTTAACTTTCTTAATATGTATCTTTGTTGCTTTATG 798  
QY 781 GCTTAATTCGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 840  
DB 799 GCTTAATTCGCTTTATGTTGTTATCTGAAGATTAATATGACAGATGAGAAACAATCA 858  
QY 841 TTGATGATTTATTCACAGATTTTAACTTAATCAAGTCACTTTTCAAAAATTTGATTTT 900  
DB 859 TTGATGATTTATTCACAGATTTTAACTTAATCAAGTCACTTTTCAAAAATTTGATTTT 918  
QY 901 TTTAATATTAATTAAGTCTGATATTCAAATGATGCTACATTTTAAATTTATGTTCAAC 960  
DB 919 TTTAATATTAATTAAGTCTGATATTCAAATGATGCTACATTTTAAATTTATGTTCAAC 978  
QY 961 TGTGTTGAGACTGAAT 977  
DB 979 TGTGTTGAGACTGAAT 995

RESULT 14  
US-10-211-462-51

; Sequence 51, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Bae Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230

SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 51  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-211-462-51

Query Match 99.3%; Score 972.2; DB 7; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
1  GGAGGCTCTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG 60
19  GGAGGCTCTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG 78
61  GGCTGTGATTCGTGCTCTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120
79  GGCTGTGATTCGTGCTCTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 138
121  CAACAGAAATTAAGCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
139  CAACAGAAATTAAGCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 198
181  TACTTCTCCGTTACTACTACGACAGGTACACGACAGGCTGCGCGAGTCTGCTGCTGCTG 240
199  TACTTCTCCGTTACTACTACGACAGGTACACGACAGGCTGCGCGAGTCTGCTGCTGCTG 258
241  GCTGCGAGGCGACCGCAACATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGCTGCA 300
259  GCTGCGAGGCGACCGCAACATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGCTGCA 318
301  GGATTAAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 360
319  GGATTAAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 378
361  GATCCACAGAAAGATTTCTTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 420
379  GATCCACAGAAAGATTTCTTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 438
421  GTGGGTGTCAACCGGACCGGATTTGAGAACAGTTTCCAGATGAGCTTCTGTATGGGCT 480
439  GTGGGTGTCAACCGGACCGGATTTGAGAACAGTTTCCAGATGAGCTTCTGTATGGGCT 498
481  TCTGGGCAACCAAGAAATTTCAATTTTGTCTAAGTTCGCAAGATGAGAGAGCTGTCT 540
499  TCTGGGCAACCAAGAAATTTCAATTTTGTCTAAGTTCGCAAGATGAGAGAGCTGTCT 558
541  CTGCGAATGTGACTGCTATTTAATTTCAAGATGAGAGCTGTGATGCTTCACT 600
559  CTGCGAATGTGACTGCTATTTAATTTCAAGATGAGAGCTGTGATGCTTCACT 618
601  AATAGCTGTGAGAGGAGATGCAATTAATTTGATGAGAGGAGATTTGCAACCTGTGAT 660
619  AATAGCTGTGAGAGGAGATGCAATTAATTTGATGAGAGGAGATTTGCAACCTGTGAT 678
661  GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCGCAAGCTTGTGCTGCTGCTGCTGCT 720
679  GTGCAAAAGCTTTGAAAAGAAAAGAAAGATGCGCAAGCTTGTGCTGCTGCTGCTGCT 738
721  GGAATAATCGAAGAAAGATTTTAACATTTCTAATATGTCATCTTGTGTGCTTTTANG 780
739  GGAATAATCGAAGAAAGATTTTAACATTTCTAATATGTCATCTTGTGTGCTTTTANG 798
781  GCTTATTTGCTTTATGTTGTATCTGAAGATTAATGACAGATGAGAGAAACAAATCA 840
799  GCTTATTTGCTTTATGTTGTATCTGAAGATTAATGACAGATGAGAGAAACAAATCA 858
841  TTGGTGATTTATTCACAGTTTATTAATTAAGATGCTTTTCAAAATTTTGAATTT 900
859  TTGGTGATTTATTCACAGTTTATTAATTAAGATGCTTTTCAAAATTTTGAATTT 918
901  TTTATATTAATTAAGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 960
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DB 919  TTTATATTAATTAAGCTGCTATTCAAATGTGAGTCAACATTTTAAATTTATGTTCAAC 978
QY 961  TTTTGTGAGCTGAT 977
DB 979  TTTTGTGAGCTGAT 995
```

## RESULT 15

US-10-956-157-1625  
Sequence 1625, Application US/10956157  
Publication No. US20050118625A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH  
FILE REFERENCE: 031896-043000 (AM 101081)  
CURRENT APPLICATION NUMBER: US/10/956,157  
CURRENT FILING DATE: 2004-10-04  
NUMBER OF SEQ ID NOS: 319805  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 1625  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-956-157-1625

Query Match 99.3%; Score 972.2; DB 9; Length 1142;  
Best Local Similarity 99.7%; Pred. No. 1.9e-245;  
Matches 974; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
1  GGAGGCTCTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG 60
19  GGAGGCTCTGGCCAGCGGCGCGCCGACCCCTGACACATGAGACCCCGCTGCGCCCTGCG 78
61  GGCTGTGATTCGTGCTCTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 120
79  GGCTGTGATTCGTGCTCTTTCTGACGAGAGCTGCACTGGGCGATGCTGCTCAGAGAGC 138
121  CAACAGAAATTAAGCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
139  CAACAGAAATTAAGCGGAGATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 198
181  TACTTCTCCGTTACTACTACGACAGGTACACGACAGGCTGCGCGAGTCTGCTGCTGCTG 240
199  TACTTCTCCGTTACTACTACGACAGGTACACGACAGGCTGCGCGAGTCTGCTGCTGCTG 258
241  GCTGCGAGGCGACCGCAACATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGCTGCA 300
259  GCTGCGAGGCGACCGCAACATTTCTACCTGAGAGGCTTGCAGAGATGCTGCTGCTGCA 318
301  GGATTAAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 360
319  GGATTAAGAAAGTTTCCCAAGTTTCCCGCTGCAAGTGAAGTGAAGCAAGTGTGAGG 378
361  GATCCACAGAAAGATTTCTTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 420
379  GATCCACAGAAAGATTTCTTTAATCTAAGTTCATGACATGTAAGAAATTTCTTTCCG 438
421  GTGGGTGTCAACCGGACCGGATTTGAGAACAGTTTCCAGATGAGCTTCTGTATGGGCT 480
439  GTGGGTGTCAACCGGACCGGATTTGAGAACAGTTTCCAGATGAGCTTCTGTATGGGCT 498
481  TCTGGGCAACCAAGAAATTTCAATTTTGTCTAAGTTCGCAAGATGAGAGAGCTGTCT 540
499  TCTGGGCAACCAAGAAATTTCAATTTTGTCTAAGTTCGCAAGATGAGAGAGCTGTCT 558
541  CTGCGAATGTGACTGCTATTTAATTTCAAGATGAGAGCTGTGATGCTTCACT 600
559  CTGCGAATGTGACTGCTATTTAATTTCAAGATGAGAGCTGTGATGCTTCACT 618
601  AATAGCTGTGAGAGGAGATGCAATTAATTTGATGAGAGGAGATTTGCAACCTGTGAT 660
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Db      619 ATACTGGCTGTGAGGGAATGCAATTAACCTTGTAGCAGGAGGATTCGAAACGTGCAT 678
Qy      661 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTGGCTTTGCCAGTAGAATCC 720
        |||
Db      679 GTGCAAAAGCTTTGAAAAAGAAAAGAGATGCCAAAGCTTGGCTTTGCCAGTAGAATCC 738
Qy      721 GGAATAATTCGAGAGAGCAATTTTAAACATCTTAATATGTCACTTGTGTCTTTATG 780
        |||
Db      739 GGAATAATTCGAGAGAGCAATTTTAAACATCTTAATATGTCACTTGTGTCTTTATG 798
Qy      781 GCTTATTTGCCCTTTATGTGTGTATCTGAAGATATATATGACAGCATGAGAAACAAATCA 840
        |||
Db      799 GCTTATTTGCCCTTTATGTGTGTATCTGAAGATATATATGACAGCATGAGAAACAAATCA 858
Qy      841 TTGATGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 900
        |||
Db      859 TTGATGATTTATTCACCAATTTTATTAATACAGTCACTTTTCAAAAATTGGATTT 918
Qy      901 TTTATATATTAACCTGCTATTTCAAAAGTGAAGTCTACCAATTTTAAATTATGTTCAC 960
        |||
Db      919 TTTATATATTAACCTGCTATTTCAAAAGTGAAGTCTACCAATTTTAAATTATGTTCAC 978
Qy      961 TGTTTGTGAGACTGAAT 977
        |||
Db      979 TGTTTGTGAGAGCAAT 995

```

Search completed: March 11, 2006, 06:24:56  
 Job time : 992 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2006, 06:08:25 ; Search time 437 Seconds  
(without alignments)  
5168.979 Million cell updates/sec

Title: US-10-800-057-1

Perfect score: 979  
1 ggaagccttgccagcgagc.....ctgttctgagactgaattc 979

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%  
Maximum March 100%  
Listing first 45 summaries

Published Applications NA New:  
1: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/FCI\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	72.3	708	US-10-821-234-546	Sequence 546, App
2	82	8.4	82	US-10-310-914A-5835	Sequence 5835, App
3	82	8.4	82	US-10-310-914A-5873	Sequence 5873, App
4	67	6.8	1647	US-11-137-465-14	Sequence 14, App1
5	59	6.0	915	US-10-821-234-668	Sequence 668, App
6	56.8	5.8	1280	US-11-000-463-214	Sequence 214, App
7	56.8	5.8	1413	US-11-177-506-2	Sequence 2, App1
8	56.8	5.8	1464	US-11-000-463-686	Sequence 686, App
9	52.6	5.4	1234	US-11-128-061-869	Sequence 869, App
10	52.6	5.4	1234	US-11-128-061-8511	Sequence 8511, App
11	52.6	5.4	1234	US-11-128-049-869	Sequence 869, App
12	52.6	5.4	1234	US-11-128-049-4511	Sequence 4511, App
13	52	5.3	600	US-11-128-061-6860	Sequence 6860, App
14	52	5.3	600	US-11-128-049-6860	Sequence 6860, App
15	52	5.3	650	US-11-128-061-3218	Sequence 3218, App
16	52	5.3	650	US-11-128-049-3218	Sequence 3218, App
17	49.2	5.0	1171	US-11-136-527-47	Sequence 47, App1
18	48.8	5.0	3994	US-11-136-527-210	Sequence 210, App
19	47.8	4.9	512	US-09-925-065A-164636	Sequence 164636, App
20	47.8	4.9	2292	US-10-821-234-767	Sequence 767, App

21	47.8	4.9	3727	US-11-091-883-22	Sequence 22, App1
22	47.8	4.9	3727	US-11-091-883-168	Sequence 168, App
23	47.2	4.8	835	US-11-128-061-96	Sequence 96, App
24	47.2	4.8	835	US-11-128-061-3738	Sequence 3738, App
25	47.2	4.8	835	US-11-128-049-96	Sequence 96, App1
26	47.2	4.8	835	US-11-128-049-3738	Sequence 3738, App
27	43.2	4.4	404	US-11-108-172-289	Sequence 289, App
28	43.2	4.4	404	US-10-821-234-271	Sequence 271, App
29	42.6	4.4	751	US-09-925-065A-66413	Sequence 66413, App
30	42.4	4.3	1267	US-10-750-185-24917	Sequence 24917, App
31	42.4	4.3	1267	US-10-750-623-24917	Sequence 24917, App
32	42.2	4.3	751	US-09-925-065A-8627	Sequence 8627, App
33	42.2	4.3	7304	US-10-240-708-78	Sequence 43, App1
34	41.6	4.2	5915	US-10-240-708-43	Sequence 78, App1
35	41.6	4.2	8961	US-10-240-708-80	Sequence 80, App1
36	41	4.2	570	US-09-925-065A-167188	Sequence 167188, App
37	41	4.2	570	US-09-925-065A-167189	Sequence 167189, App
38	41	4.2	783	US-11-234-786-15	Sequence 15, App1
39	40.6	4.1	570	US-09-925-065A-167190	Sequence 167190, App
40	40.4	4.1	552	US-09-925-065A-463533	Sequence 463533, App
41	40.4	4.1	552	US-09-925-065A-436635	Sequence 436635, App
42	40.2	4.1	607	US-09-925-065A-436635	Sequence 436635, App
43	40.2	4.1	636	US-09-925-065A-727350	Sequence 727350, App
44	40.2	4.1	19233	US-10-240-708-45	Sequence 45, App1
45	40.2	4.1	163317	US-11-117-187-212	Sequence 212, App

## ALIGNMENTS

RESULT 1					
US-10-821-234-546					
Sequence 546, Application US/10821234					
Publication No. US20050255114A1					
GENERAL INFORMATION:					
APPLICANT: Labat, Ivan					
APPLICANT: Stache-Crain, Birgit					
APPLICANT: Andaman, Susan					
APPLICANT: Tang, Y. Tom					
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia					
FILE REFERENCE: 821A					
CURRENT APPLICATION NUMBER: US/10/821,234					
CURRENT FILING DATE: 2004-04-07					
PRIOR APPLICATION NUMBER: US 60/462,047					
PRIOR FILING DATE: 2003-04-07					
NUMBER OF SEQ ID NOS: 1704					
SOFTWARE: pc_sro_genes Version 1.0					
SEQ ID NO 546					
LENGTH: 708					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-10-821-234-546					
Query Match					
Best Local Similarity, 100.0%; Pred. No. 44e-151; Indels 0; Gaps 0;					
Matches 708; Conservative 0; Mismatches 0;					
QY	39	ATGACCCCGCTGCGCCCTGCGGCTGTCATTCGTGCTTTCTTGACGAGGCTGCA	98		
DB	1	ATGACCCCGCTGCGCCCTGCGGCTGTCATTCGTGCTTTCTTGACGAGGCTGCA	60		
QY	99	CTGGCGGATGCTGCTCAGAGCCAAAGAAATTAACGGAGATCTGCTCGCCCTTA	158		
DB	61	CTGGCGGATGCTGCTCAGAGCCAAAGAAATTAACGGAGATCTGCTCGCCCTTA	120		
QY	159	GACTACGAGCCCTGCGGAGGCTGCTTCTCGCTTACTACTACGAGGTAACGAGAGC	218		
DB	121	GACTACGAGCCCTGCGGAGGCTGCTTCTCGCTTACTACTACGAGGTAACGAGAGC	180		
QY	219	TGCGCGGATGCTGCTCAGAGGCTGCGAGGCAACGCAATTTTACACCTGGAGG	278		
DB	181	TGCGCGGATGCTGCTCAGAGGCTGCGAGGCAACGCAATTTTACACCTGGAGG	240		

QY 279 GCTTGACGACGATGCTTGCTGAGATGATAAAAAAGTTCCCAAGTTGGCCGCGCTGCAGATG 338  
DB 241 GCTTGACGACGATGCTTGCTGAGATGATAAAAAAGTTCCCAAGTTGGCCGCGCTGCAGATG 300  
QY 339 AGTGTGACGACGATGCTTGCTGAGATGATAAAAAAGTTCCCAAGTTGGCCGCGCTGCAGATG 398  
DB 301 AGTGTGACGACGATGCTTGCTGAGATGATAAAAAAGTTCCCAAGTTGGCCGCGCTGCAGATG 360  
QY 399 ACATGTGAAAAATTTCTTTCCGCTGGGTGTCAACCGGAACCGGATGAGAACAGATTTCCA 458  
DB 361 ACATGTGAAAAATTTCTTTCCGCTGGGTGTCAACCGGAACCGGATGAGAACAGATTTCCA 420  
QY 459 GATGAACTGATCTGTATGAGGCTTTCTGCGCACAAGAAAAATTCATCATTTTGTCTACAGT 518  
DB 421 GATGAACTGATCTGTATGAGGCTTTCTGCGCACAAGAAAAATTCATCATTTTGTCTACAGT 480  
QY 519 CCAAAAAGATGAGGAGCTGTGCTGCTGCAATGTGACTCGCTATTTATTTAATCCAAAGATG 578  
DB 481 CCAAAAAGATGAGGAGCTGTGCTGCTGCAATGTGACTCGCTATTTATTTAATCCAAAGATG 540  
QY 579 AGAACCTGTGATGCTTTCACTATACCTGCTGTGAGGAGATGACAATTTTGTAGC 638  
DB 541 AGAACCTGTGATGCTTTCACTATACCTGCTGTGAGGAGATGACAATTTTGTAGC 600  
QY 639 AGGAGGATGCAACGTCGATGTGCAAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAG 698  
DB 601 AGGAGGATGCAACGTCGATGTGCAAAAAGCTTTGAAAAAGAAAAAGAGATGCCAAG 660  
QY 699 CTTGCTTTGCCAGTATGATCGGAAAAATTCGGAAGAACATTTTAA 746  
DB 661 CTTGCTTTGCCAGTATGATCGGAAAAATTCGGAAGAACATTTTAA 708

## RESULT 2

US-10-310-914A-5835  
; Sequence 5835, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200, CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5835  
; LENGTH: 82  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-5835

Query Match 8.4%; Score 82; DB 8; Length 82;  
Best Local Similarity 76.8%; Pred. No. 2.5e-09;  
Matches 63; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCTACACCTGGAGGCTTGGCGACGATGCTTGCTGAGATGAAAAAGTTCCCAAGTTT 324  
DB 1 UCUCACCTGGAGGCTTGGCGACGATGCTTGCTGAGATGAAAAAGTTCCCAAGTTT 60  
QY 325 GCCGCTGCAAGTGTGGA 346  
DB 61 GCCGCTGCAAGTGTGGA 82

## RESULT 3

US-10-310-914A-5873  
; Sequence 5873, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiller, Kiyuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087, 0200, CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5873  
; LENGTH: 82  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-5873

Query Match 8.4%; Score 82; DB 8; Length 82;  
Best Local Similarity 76.8%; Pred. No. 2.5e-09;  
Matches 63; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

QY 265 TCTACACCTGGAGGCTTGGCGACGATGCTTGCTGAGATGAAAAAGTTCCCAAGTTT 324  
DB 1 UCUCACCTGGAGGCTTGGCGACGATGCTTGCTGAGATGAAAAAGTTCCCAAGTTT 60  
QY 325 GCCGCTGCAAGTGTGGA 346  
DB 61 GCCGCTGCAAGTGTGGA 82

## RESULT 4

US-11-137-465-14  
; Sequence 14, Application US/11137465  
; Publication No. US20050255558A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia, K.  
; APPLICANT: Smith, Randall, P.  
; APPLICANT: Xiang, Zhaoxing  
; APPLICANT: Kadnick, Karen  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50018  
; CURRENT APPLICATION NUMBER: US/11/137,465  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US/10/239,663  
; PRIOR FILING DATE: 2002-09-24  
; PRIOR APPLICATION NUMBER: PCT/US01/09226  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/192,158  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/192,668  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: 60/200,166  
; PRIOR FILING DATE: 2000-04-27  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-137-465-14

Query Match 6.8%; Score 67; DB 12; Length 1647;  
Best Local Similarity 63.2%; Pred. No. 1.8e-05;  
Matches 103; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 134 CGCGAGATCTGTCTCCGCCCCCTAGACTAGACCCCTGCGGCGCCCTACTTCCCTTA 193  
DB 1065 CGCGAGATCTGTCTCCGCCCCCTAGACTAGACCCCTGCGGCGCCCTACTTCCCTTA 1124  
QY 194 CTACTACGACGATGACGACGAGCTGCGGCACTTCTGTACCGGCGCTGCGAGGCA 253  
DB 1125 GCGCTACGACCGGCTGCTGACGAGCTGCAATCCCTCTGTACCGGCTGCGAGGCA 1184  
QY 254 CGCGAATTTCTACCTGAGAGGCTTGGAGAGATGCTTG 296

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 9, 2006, 19:49:24 ; Search time 189 Seconds  
(without alignments)  
546.318 Million cell updates/sec

Title: US-10-800-057-2  
Perfect score: 1306  
Sequence: 1 MDPARPLGSLILFLTEAA.....KKMPKLRFAFRIRKIKKQF 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: geneseqp1980a:\*  
2: geneseqp1980a:\*  
3: geneseqp2000a:\*  
4: geneseqp2001a:\*  
5: geneseqp2002a:\*  
6: geneseqp2003a:\*  
7: geneseqp2003a:\*  
8: geneseqp2004a:\*  
9: geneseqp2005a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	2 AAR74977	AAR74977 Human Kun
2	1306	100.0	235	4 AAB76856	AAB76856 Human Lun
3	1306	100.0	235	5 ABG96429	ABG96429 Human Ova
4	1306	100.0	235	5 AAU85511	AAU85511 Clone #19
5	1306	100.0	235	5 ABP68618	ABP68618 Human Pan
6	1306	100.0	235	6 ABU03481	ABU03481 Angiogene
7	1306	100.0	235	6 ABUS6599	ABUS6599 Lung can
8	1306	100.0	235	6 ABUS6599	ABUS6599 Lung can
9	1306	100.0	235	6 ABUS6599	ABUS6599 Lung can
10	1306	100.0	235	6 ABUS6599	ABUS6599 Lung can
11	1306	100.0	235	7 ADH45851	ADH45851 Human Lun
12	1306	100.0	235	7 ADH45851	ADH45851 Human Lun
13	1306	100.0	235	7 ADH45851	ADH45851 Human Lun
14	1306	100.0	235	8 ADL83255	ADL83255 Human PRO
15	1306	100.0	235	8 ADL83255	ADL83255 Human PRO
16	1306	100.0	235	8 ADU06660	ADU06660 Novel bro
17	1306	100.0	235	8 ADU06660	ADU06660 Novel bro
18	1290	98.8	245	8 ABM83218	ABM83218 Human tis
19	1200	91.9	213	6 AAW61535	AAW61535 Human tis
20	1200	91.9	213	6 ABU07725	ABU07725 Human tis
21	1136.5	87.0	210	4 AAU02970	AAU02970 Angiotens
22	1126.5	86.3	211	4 AAU02969	AAU02969 Angiotens
23	986	75.5	188	4 AAU02979	AAU02979 Angiotens
24	464	35.5	88	6 ABR39435	ABR39435 Human GEN

25	394.5	30.2	291	6 ABR48476	ABr48476 Human Tif
26	393.5	30.1	291	6 ABR48478	ABr48478 Human Tif
27	388	29.7	304	2 AAR67994	AAR67994 Tissue fa
28	388	29.7	304	2 AAR61884	AAR61884 Lipoprote
29	388	29.7	304	2 AAY49557	AAY49557 Human lip
30	388	29.7	304	2 ADT09568	ADT09568 Human tis
31	388	29.7	304	8 ADQ88030	ADQ88030 Human ser
32	388	29.7	304	8 ADL14411	ADL14411 Human NF-
33	388	29.7	304	8 ADU06597	ADU06597 Novel bro
34	388	29.7	304	8 ADU73579	ADU73579 Human tis
35	388	29.7	304	9 ADY36969	ADY36969 Human ser
36	388	29.7	304	9 ADY82826	ADY82826 Human ser
37	387.5	29.7	276	2 AAR92012	AAR92012 TPPI mute
38	387.5	29.7	276	2 AAR92265	AAR92265 TPPI mute
39	387	29.6	304	2 AAR8389	AAR8389 Human lip
40	384.5	29.4	276	2 AAW30311	AAW30311 Recombina
41	384.5	29.4	276	2 AAW61535	AAW61535 Human tis
42	384.5	29.4	276	6 ABU07724	ABU07724 Human tis
43	384.5	29.4	276	7 ADE80824	ADE80824 Human tis
44	384.5	29.4	276	7 ADE80822	ADE80822 Human tis
45	384.5	29.4	276	7 ADI20097	ADI20097 Human TFP

## ALIGNMENTS

RESULT 1  
AAR74977 standard, protein, 235 AA.

AC AAR74977;  
XX 21-JUN-1996 (first entry)  
XX Human Kunitz-type protease-inhibitor TPPI-2.  
DE Human Kunitz-type protease-inhibitor TPPI-2.  
XX Kunitz-type inhibitor; protease-inhibitor; enzyme-inhibitor;  
KW antioagulant; deep vein thrombosis.  
XX Homo sapiens.  
OS  
XX  
XX W09512674-A1.  
XX  
XX 11-MAY-1995.  
XX  
XX 02-NOV-1994; 94WO-US012609.  
XX  
XX 05-NOV-1993; 93US-00147710.  
XX  
XX (ZYMO) ZYMOGENETICS INC.  
XX (UTNE-) UNIV NEW MEXICO STATE.  
XX Sprecher CA, Kistiel W, Foster DC;  
XX WPI; 1995-193821/25.  
XX N-FSDB; AAQ90469.  
XX  
XX Human Kunitz-type protease inhibitors - used as antioagulant and in the  
XX treatment of deep vein thrombosis.  
XX  
XX Claim 2; Page 50; 65pp; English.  
XX  
XX KTI is used to inhibit blood coagulation in mammals. It is particularly  
XX used as an antioagulant and in the treatment of deep vein thrombosis,  
XX disseminated intravascular coagulations, pulmonary embolism and in the  
XX prevention of thrombosis following surgery. KTI inhibits Factor-VIII in  
XX the absence of Factor-Xa, and thus does not require production of Factor-  
XX Xa via the intrinsic or extrinsic pathway. This KTI protein shares AA  
XX sequence homology and overall domain organization with tissue factor  
XX pathway-inhibitor (TFPI), and has therefore been designated TPPI-2  
XX Sequence 235 AA;



Query Match 100.0%; Score 1306; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
QY 61 CROFLYGCGEGNANNFYTWACDCAWRIEKVPCRLQVSDQCEGSTKRYFNLSSM 120  
DB 61 CROFLYGCGEGNANNFYTWACDCAWRIEKVPCRLQVSDQCEGSTKRYFNLSSM 120  
QY 121 TCCKPFGSGCHNRRIENRPDEATCMGFCAPKPIPSFCYSPDEGLCSANVTYYFNPRY 180  
DB 121 TCCKPFGSGCHNRRIENRPDEATCMGFCAPKPIPSFCYSPDEGLCSANVTYYFNPRY 180  
QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

## RESULT 2

AAB76856  
ID AAB76856 standard; protein; 235 AA.  
XX AAB76856;

12-APR-2001 (first entry)

Human lung tumour protein related protein sequence SEQ ID NO:332.

Human; lung cancer; lung tumour; lung tumour protein; gene therapy;  
lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;  
cytostatic; anticancer; antisense inhibition.

Homo sapiens.

MO200100828-A2.

04-JAN-2001.

30-JUN-2000; 2000MO-US018061.

30-JUN-1999; 99US-00346492.

15-OCT-1999; 99US-00419356.

17-DEC-1999; 99US-00466867.

30-DEC-1999; 99US-00476300.

06-MAR-2000; 2000US-00519642.

22-MAR-2000; 2000US-00533077.

10-APR-2000; 2000US-00546259.

27-APR-2000; 2000US-00560406.

05-JUN-2000; 2000US-00589184.

(COR-) CORIXA CORP.

Wang T, Bangur GS, Lodes MJ, Fanger GR, Vedvick TS, Carter D,  
Rettler MW, Mannion J;

WPI; 2001-071488/08.

Example 1; Page 260-261; 436P; English.

The present invention describes immunogenic portions of lung tumour-  
associated proteins (I) and the nucleic acids (NA) that encode them. (I)  
have cytostatic activity and can be used in gene therapy, antisense  
inhibition and in vaccines. The NAs and the lung tumour-associated  
proteins they encode may be used in the prevention, treatment and  
diagnosis of diseases associated with their inappropriate expression,  
especially lung cancers. For example, the NAs may be administered to  
treat diseases by rectifying mutations or deletions in a patient's genome

CC that affect the activity of the protein by expressing inactive proteins  
CC or to supplement the patient's own production of (I). Additionally, the  
CC NAs may be used to produce the lung-tumour associated protein, according  
CC to standard recombinant DNA methodology. Conversely, antisense NA  
CC molecules may be administered to down regulate protein expression by  
CC binding with the cells own genes and preventing their expression. The NA  
CC and complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar NA sequences in  
CC samples, and hence which patients may be in need of treatment for lung  
CC cancer. The (I) may be used as antigens in the production of antibodies  
CC and in assays to identify modulators (agonists and antagonists) of the  
CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848  
CC to AAB76878 represent human lung tumour protein related nucleotide and  
CC protein sequences which are used in the exemplification of the present  
CC invention  
XX

Sequence 235 AA;

Query Match 100.0%; Score 1306; DB 4; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60  
DB 1 MDPARPLGSLILLFLTEALGDAOEPGNNAEICLLPLDYGPCRALIRYYDRYTOS 60

QY 61 CROFLYGCGEGNANNFYTWACDCAWRIEKVPCRLQVSDQCEGSTKRYFNLSSM 120  
DB 61 CROFLYGCGEGNANNFYTWACDCAWRIEKVPCRLQVSDQCEGSTKRYFNLSSM 120

QY 121 TCCKPFGSGCHNRRIENRPDEATCMGFCAPKPIPSFCYSPDEGLCSANVTYYFNPRY 180  
DB 121 TCCKPFGSGCHNRRIENRPDEATCMGFCAPKPIPSFCYSPDEGLCSANVTYYFNPRY 180

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

QY 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235  
DB 181 RTCDAPFTYTCGGGNDNNFVSRBDCRACAKALKKKKKMPRLRPAIRIRIRKKQF 235

PA (MILL-) MILLENNIUM PHARM INC.  
XX Monahan JE, Gamaavarapu M, Hoersch S, Kamathar S, Kovacic SG,  
PI Meyers RE, Morrissey MP, Olandt PJ, Sen A, Vleby PO, Mills GB,  
PI Baat RC, Lu K, Schmandt RE, Zhao X, Glatt K;  
XX WPI: 2002-72377/78.  
DR N-P8DB; AB876528.  
XX  
XX Assessing whether a patient is afflicted with ovarian cancer, useful in  
PT assessing the stage or progression of the disease, comprises comparing  
PI the expression level of a cancer marker in a sample from a patient and  
PT from a non cancer patient.  
XX  
XX Disclosure; Page 437-438; 481pp; English.  
XX  
XX The present invention relates to a new method for assessing whether a  
CC patient is afflicted with ovarian cancer. The method involves comparing  
CC the expression level of a marker in a patient sample and the normal level  
CC of expression of the marker in a control non-ovarian cancer sample, where  
CC the marker is selected from 363 cancer markers described in the  
CC specification. The method of the invention is useful in diagnosing or  
CC characterizing cancer, in detecting the presence of cancer as early as  
CC possible, and the recurrence of ovarian cancer. The method may also be of  
CC particular use with patients having an enhanced risk of developing  
CC ovarian cancer (e.g. patients having a familial history of ovarian  
CC cancer). The cancer markers may be used in the management and treatment  
CC of e.g. brain and central nervous system disorders (e.g. bacterial and  
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain  
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),  
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),  
CC testicular disorders (e.g. nonbacterial granulomatous orchitis),  
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart  
CC disease or atherosclerosis). The compositions and methods may also be  
CC used in assessing the histological type of neoplasm associated with  
CC ovarian cancer, monitoring the progression of ovarian cancer, determining  
CC whether ovarian cancer has metastasized or is likely to metastasize,  
CC selecting a composition for inhibiting ovarian cancer, assessing the  
CC ovarian carcinogenic potential of a compound, or inhibiting ovarian  
CC cancer or at risk of developing ovarian cancer. The present amino acid  
CC sequence represents one of the ovarian cancer markers described in the  
CC invention  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSIILLPTTEALGDAAOEPGNNABICLLPLDYGPCALLRYYDRYTOS 60  
DB 1 MDPAPPLGSIILLPTTEALGDAAOEPGNNABICLLPLDYGPCALLRYYDRYTOS 60  
QY 61 CROPLFGGCEGNANNFYTWBACDCAWRIEKPVKYCRLOVSVDQCEGSTEKTFPULSSM 120  
DB 61 CROPLFGGCEGNANNFYTWBACDCAWRIEKPVKYCRLOVSVDQCEGSTEKTFPULSSM 120  
QY 121 TCEKFPSSGCHNRRIENRPPDEATCGFCAPKKIPSCYSPXOBGLCSANVTRYENPRY 180  
DB 121 TCEKFPSSGCHNRRIENRPPDEATCGFCAPKKIPSCYSPXOBGLCSANVTRYENPRY 180  
QY 181 RTCDATYTYGCGGNDNPFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
DB 181 RTCDATYTYGCGGNDNPFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
RESULT 4  
AAU85511  
ID AAU85511 standard, protein, 235 AA.  
XX AAU85511;  
XX  
XX 21-MAY-2002 (first entry)

XX Clone #19117 of lung tumour protein.  
DE  
XX Lung tumour; cancer; T cell; immune response stimulator; cytostatic.  
XX  
XX Homo sapiens.  
OS  
XX WO200204514-A2.  
XX  
XX 17-JAN-2002.  
XX  
XX 10-JUL-2001; 2001WO-US022058.  
XX  
XX 11-JUL-2000; 2000US-00614124.  
XX 29-AUG-2000; 2000US-00651553.  
XX 08-SEP-2000; 2000US-00658824.  
XX 26-SEP-2000; 2000US-00671325.  
XX 06-OCT-2000; 2000US-00677419.  
XX 30-OCT-2000; 2000US-00702705.  
XX 13-DEC-2000; 2000US-00736457.  
XX 03-MAY-2001; 2001US-00849626.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Matanabe Y, Henderson RA, Johnson JC, Retter MM;  
PI Marnerakis M, Carter D, Fanger GR, Vedgick TS, Bangur CS, Menabb A;  
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;  
XX WPI: 2002-164634/21.  
DR N-P8DB; ABK38057.  
XX  
XX Novel polynucleotide encoding a lung tumor polypeptide useful for  
PT stimulating and/or expanding T cells specific for a tumor protein.  
XX  
XX Example 1; SEQ ID NO 332; 223pp; English.  
XX  
XX The invention describes an isolated polynucleotide and polypeptide useful  
CC for stimulating and/or expanding T cells specific for a tumor protein  
CC for determining the presence of a cancer in a patient. A composition  
CC containing the polynucleotide and/or polypeptide is useful for treating a  
CC lung cancer in a patient. The polypeptide is useful for removing tumour  
CC cells from a biological sample. The polynucleotide is also useful as  
CC a probe or primer to detect the level of mRNA encoding a tumour protein.  
CC This is the amino acid sequence of a lung tumour associated protein.  
CC described in the method of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGSIILLPTTEALGDAAOEPGNNABICLLPLDYGPCALLRYYDRYTOS 60  
DB 1 MDPAPPLGSIILLPTTEALGDAAOEPGNNABICLLPLDYGPCALLRYYDRYTOS 60  
QY 61 CROPLFGGCEGNANNFYTWBACDCAWRIEKPVKYCRLOVSVDQCEGSTEKTFPULSSM 120  
DB 61 CROPLFGGCEGNANNFYTWBACDCAWRIEKPVKYCRLOVSVDQCEGSTEKTFPULSSM 120  
QY 121 TCEKFPSSGCHNRRIENRPPDEATCGFCAPKKIPSCYSPXOBGLCSANVTRYENPRY 180  
DB 121 TCEKFPSSGCHNRRIENRPPDEATCGFCAPKKIPSCYSPXOBGLCSANVTRYENPRY 180  
QY 181 RTCDATYTYGCGGNDNPFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
DB 181 RTCDATYTYGCGGNDNPFVSRBCKRAKAKLKKKKMPKLRPASIRIKRKQF 235  
RESULT 5

ABP68618  
ID ABP68618 standard; protein; 235 AA.  
XX  
AC ABP68618;  
XX  
DT 14-JAN-2003 (first entry)  
XX  
DE Human pancreatic cancer expressed protein SEQ ID NO 167.  
XX  
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
XX  
KW cytostatic; tumour.  
XX  
OS Homo sapiens.  
XX  
PN WO200260317-A2.  
XX  
PD 08-AUG-2002.  
XX  
PP 30-JAN-2002; 2002WO-US002781.  
XX  
PR 30-JAN-2001; 2001US-0265305P.  
XX  
PR 31-JAN-2001; 2001US-0265682P.  
XX  
PR 09-FEB-2001; 2001US-0267568P.  
XX  
PR 21-MAR-2001; 2001US-0279651P.  
XX  
PR 28-APR-2001; 2001US-0287112P.  
XX  
PR 16-MAY-2001; 2001US-0291631P.  
XX  
PR 12-JUL-2001; 2001US-0305484P.  
XX  
PR 20-AUG-2001; 2001US-0313999P.  
XX  
PR 27-NOV-2001; 2001US-0333626P.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Benson DR, Kalos MD, Iodes MJ, Persing DH, Hapler WT, Jiang Y;  
XX  
DR WPI; 2002-627435/67.  
XX  
DR N-PSDB; ABV94764.  
XX  
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
XX  
PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
XX  
PT cancer.  
XX  
PS Claim 2; SEQ ID NO 167; 300pp + Sequence Listing; English.  
XX  
XX  
CC The invention relates to an isolated polynucleotide (1) comprising: (a)  
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
CC complements of (a); (c) sequences consisting of at least 20 contiguous  
CC residues of (a); (d) sequences that hybridize to (a), under moderately  
CC stringent conditions; (e) sequences having at least 75% or 90% identity  
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68536-  
CC ABP68637) encoded by (1) and oligonucleotide can be used to detect cancer  
CC in a patient and compositions comprising polypeptides, polynucleotides,  
CC antibodies, fusion proteins, T cell populations and antigen presenting  
CC cells expressing the polypeptide are useful in treating pancreatic cancer  
CC and stimulating an immune response. The polynucleotide can be used as  
CC probes or primers for nucleic acid hybridization, in the design and  
CC preparation of ribozyme molecules for inhibiting expression of the tumour  
CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
CC therapy. Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
SQ Sequence 235 AA;  
XX

Query Match 100.0%; Score 1306; DB 5; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MDPAPPLGSLILPLTEAALGDAAGPTGNNALICLPLDYGPCRALLRYYDRYQS 60  
1 MDPAPPLGSLILPLTEAALGDAAGPTGNNALICLPLDYGPCRALLRYYDRYQS 60  
1 MDPAPPLGSLILPLTEAALGDAAGPTGNNALICLPLDYGPCRALLRYYDRYQS 60  
61 CROFLYGGCGEANNPFTWEACDDACMRLEKVPKVCRLQVSDDCGSGTEKFFNLSM 120  
|||||

DB 61 CROFLYGGCGEANNPFTWEACDDACMRLEKVPKVCRLQVSDDCGSGTEKFFNLSM 120  
QY 121 TCEKFFSGGCHNRRIENRPPDRTGFCAPKKIFSPCYSPROEGLCSANVTRYFNPRY 180  
DB 121 TCEKFFSGGCHNRRIENRPPDRTGFCAPKKIFSPCYSPROEGLCSANVTRYFNPRY 180  
QY 181 RTCDAPFTYTGCGGNNPVSREDCCRACAKALKKKKRMPKLPASIRIRKRRQF 235  
DB 181 RTCDAPFTYTGCGGNNPVSREDCCRACAKALKKKKRMPKLPASIRIRKRRQF 235  
RESULT 6  
ABU03481  
ID ABU03481 standard; protein; 235 AA.  
XX  
AC ABU03481;  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Angiogenesis-associated human protein sequence #26.  
XX  
KW Human; angiogenesis-associated transcript; angiogenesis;  
XX  
KW angiogenesis-associated disease; cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO200279492-A2.  
XX  
PD 10-OCT-2002.  
XX  
PP 14-FEB-2002; 2002WO-US004915.  
XX  
PR 14-FEB-2001; 2001US-00784356.  
XX  
PR 22-FEB-2001; 2001US-00791390.  
XX  
PR 19-APR-2001; 2001US-0286475P.  
XX  
PR 03-AUG-2001; 2001US-0310025P.  
XX  
PR 13-NOV-2001; 2001US-0350666P.  
XX  
PR 29-NOV-2001; 2001US-0334244P.  
XX  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Murray R, Glynn R, Watson SR, Aziz N;  
XX  
DR WPI; 2003-040681/03.  
XX  
DR N-PSDB; ABX08764.  
XX  
PT Detecting angiogenesis-associated transcript in a cell for diagnosing and  
XX  
PT treating cancer by contacting a sample with a polynucleotide that  
XX  
PT exhibits changes in expression level as a function of time in tissue  
XX  
PT undergoing angiogenesis.  
XX  
PS Example 2; Page 205; 291pp; English.  
XX  
XX  
CC The present invention relates to methods and compositions for detecting  
CC an angiogenesis-associated transcript in a cell in a patient. The method  
CC involves contacting a biological sample from the patient with a  
CC polynucleotide that selectively hybridizes to a sequence at least 80%  
CC identical to any of the angiogenesis-associated human polynucleotide  
CC sequences given in the specification. These angiogenesis-associated  
CC polynucleotide sequences comprise genes that exhibit changes in  
CC expression levels as a function of time in tissue undergoing  
CC angiogenesis. The method and the polynucleotide sequences of the  
CC invention are useful for diagnosing and treating angiogenesis and  
CC angiogenesis-associated diseases e.g. cancer. The polynucleotide  
CC sequences are also useful in the gene therapy of such disorders. The  
CC angiogenesis-associated proteins encoded by the polynucleotide sequences  
CC are useful as a vaccine for therapeutic and prophylactic immunisation.  
CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences  
XX  
XX  
SQ Sequence 235 AA;  
XX

Query Match 100.0%; Score 1306; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;



PT compositions, e.g. vaccines, for treating lung cancer.  
XX  
XX Example 1; Page; 72pp; English.  
XX  
CC The invention relates to a polynucleotide encoding a lung tumour protein,  
CC comprising a sequence selected from any of the 14 sequences mentioned in  
CC the specification, or a sequence (S2) mentioned in specification,  
CC complement of S1, sequences consisting of at least 20 contiguous residues  
CC of S1, sequences that hybridise to S1, sequences having 75%, preferably  
CC 90%, identity to S1, or degenerate variants of S1. Also included are an  
CC isolated polypeptide (comprising a sequence (S3) selected from any one of  
CC the 4 amino acid sequences mentioned in the specification, a sequence  
CC encoded by the polynucleotide, or sequences having at least 70%,  
CC preferably 90%, identity to a sequence encoded by the polynucleotide), an  
CC expression vector comprising the polynucleotide operably linked to an  
CC expression control sequence, a host cell transformed or transfected with  
CC the vector, an isolated antibody (or its antigen-binding fragment) that  
CC specifically binds to the polypeptide, detecting the presence of a cancer  
CC in a patient, a fusion protein comprising the polypeptide, an  
CC oligonucleotide that hybridises to S1 under moderately stringent  
CC conditions, stimulating and/or expanding T cells specific for a tumour  
CC protein (comprising contacting T cells with the polynucleotide, protein  
CC or antigen-presenting cells, under conditions and for a time sufficient  
CC to permit the stimulation and/or expansion of T cells) and inhibiting the  
CC development of a cancer in a patient (by incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T  
CC cells isolated from a patient with the polynucleotide, protein or antigen  
CC presenting cells that express the polynucleotide, such that T cells  
CC proliferate, administering to the patient an effective amount of the  
CC proliferated T cells, and thus inhibiting the development of a cancer in  
CC the patient. The polynucleotide, protein and cells are useful in a  
CC composition for stimulating an immune response in a patient, and for  
CC treating a cancer in a patient (particularly lung cancer). The  
CC oligonucleotide is useful for determining the presence of a cancer in a  
CC patient. The protein and oligonucleotides are useful in pharmaceutical  
CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe  
CC or primer for nucleic acid hybridisation, and in the design and  
CC preparation of ribozyme molecules for inhibiting expression of tumour  
CC polypeptides and proteins in tumour cells. An amplified portion of the  
CC polynucleotide is useful for isolating a full-length gene from a suitable  
CC library. The present sequence is a protein encoded by a cDNA (full  
CC length, extended or partial) isolated from a library derived from lung  
CC tumour/ cancer cells. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from the USPTO at  
CC seqdata.uspto.gov/sequence.html?DocId=20020197669  
CC  
XX  
SQ Sequence 235 AA;  
Query Match 100.0%; Score 1306; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MDPAPRLGSLILLFLTEALGDAAQEPGNNNAICLLPLDYGPCRALLLRYRYDRTQS 60  
DB 1 MDPAPRLGSLILLFLTEALGDAAQEPGNNNAICLLPLDYGPCRALLLRYRYDRTQS 60  
OY 61 CRQFLYGGCEGNANFYWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLISM 120  
DB 61 CRQFLYGGCEGNANFYWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLISM 120  
OY 121 TCEKFPFSGGCHRRRIENRPDEATCMGFCAPKIKIPSCYSPKDBGLCSANVTTRYFNPRY 180  
DB 121 TCEKFPFSGGCHRRRIENRPDEATCMGFCAPKIKIPSCYSPKDBGLCSANVTTRYFNPRY 180  
OY 181 RTCDAFTYTGCGGNDNNFVSRDCKRAKAKLKKKKMPKLRPASIRIKIRKKOP 235  
DB 181 RTCDAFTYTGCGGNDNNFVSRDCKRAKAKLKKKKMPKLRPASIRIKIRKKOP 235  
RESULT 9  
ABU66385  
ID ABU66385 standard; protein; 235 AA.  
XX

AC ABU66385;  
XX  
XX 22-MAY-2003 (first entry)  
XX  
XX Lung cancer therapyand diagnosis associated protein #9.  
XX  
XX Lung cancer; cytostatic; vaccine; gene therapy; cancer.  
XX  
XX Homo sapiens.  
XX  
XX US2002172952-A1.  
XX  
XX 21-NOV-2002.  
XX  
XX 10-JUL-2001; 2001US-00902941.  
XX  
XX 30-JUN-1999; 99US-00346492.  
XX 15-OCT-1999; 99US-00419356.  
XX 17-DEC-1999; 99US-00468867.  
XX 30-DEC-1999; 99US-00476300.  
XX 06-MAR-2000; 2000US-00519642.  
XX 22-MAR-2000; 2000US-00533077.  
XX 10-APR-2000; 2000US-00546259.  
XX 27-APR-2000; 2000US-00560406.  
XX 05-JUN-2000; 2000US-00589184.  
XX 11-JUL-2000; 2000US-00614124.  
XX 29-AUG-2000; 2000US-00651563.  
XX 08-SEP-2000; 2000US-00658824.  
XX 26-SEP-2000; 2000US-00671325.  
XX 06-OCT-2000; 2000US-00677419.  
XX 30-OCT-2000; 2000US-00702705.  
XX 13-DEC-2000; 2000US-00736457.  
XX 03-MAY-2001; 2001US-00849626.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;  
XX Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;  
XX WPI; 2003-328427/31.  
XX  
XX New polynucleotide, useful for preparing a composition for treating or  
XX inhibiting development of cancer, e.g. lung cancer.  
XX  
XX  
XX Disclosure; SEQ ID NO 332; 82pp; English.  
XX  
XX  
XX The invention describes an isolated polynucleotide comprising one of 32  
XX sequences, complement or degenerate variants of them. The polynucleotide  
XX is useful for preparing a composition e.g. a vaccine or for gene therapy,  
XX for treating or inhibiting development of cancer, e.g. lung cancer. This  
XX sequence represents a polypeptide associated with the compositions and  
XX methods for the therapy and diagnosis of lung cancer  
XX  
SQ Sequence 235 AA;  
Query Match 100.0%; Score 1306; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MDPAPRLGSLILLFLTEALGDAAQEPGNNNAICLLPLDYGPCRALLLRYRYDRTQS 60  
DB 1 MDPAPRLGSLILLFLTEALGDAAQEPGNNNAICLLPLDYGPCRALLLRYRYDRTQS 60  
OY 61 CRQFLYGGCEGNANFYWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLISM 120  
DB 61 CRQFLYGGCEGNANFYWEACDDACWRIEKVPKVCRLQVSVDDQCEGSTEKYPFNLISM 120  
OY 121 TCEKFPFSGGCHRRRIENRPDEATCMGFCAPKIKIPSCYSPKDBGLCSANVTTRYFNPRY 180  
DB 121 TCEKFPFSGGCHRRRIENRPDEATCMGFCAPKIKIPSCYSPKDBGLCSANVTTRYFNPRY 180  
OY 181 RTCDAFTYTGCGGNDNNFVSRDCKRAKAKLKKKKMPKLRPASIRIKIRKKOP 235  
DB 181 RTCDAFTYTGCGGNDNNFVSRDCKRAKAKLKKKKMPKLRPASIRIKIRKKOP 235

DB 181 RTCDATYTCGGGNDNNFVSRBDCKRACAKALKKKKMKPLRFPASIRIRKRRKQF 235

RESULT 10

ID ADH45851 standard; protein; 235 AA.

AC ADH45851;

XX

XX

XX 25-MAR-2004 (first entry)

DT

XX Human lung tumour clone protein, SEQ ID NO 332.

DE

XX Human lung tumour; cytostatic; immunostimulant; vaccine; gene therapy;

KW human; clone.

XX

XX Homo sapiens.

OS

XX WO2003037267-A2.

PN

XX 08-MAY-2003.

PD

XX 28-OCT-2002; 2002WO-US034777.

PF

XX 29-OCT-2001; 2001US-00017754.

PR

XX 28-MAR-2002; 2002US-00113872.

PA (CORI-) CORIXA CORP.

XX

XX Henderson RA, Wang T, Watanabe Y, Kalos MD, Sleath PR;

PI Johnson JC, Retter MW, Durham M, Carter D, Fanger GR, Vedvick TS;

PI Bangur CS, McNabb A;

XX

XX WPI; 2003-468346/44.

DR

XX

XX New polypeptides and encoding polynucleotides, useful for diagnosing,

PT preventing and/or treating lung cancer.

XX

XX Example 1; SEQ ID NO 332; 258bp; English.

PS

XX The invention relates to novel compositions and methods for the therapy

XX and diagnosis of cancer, particularly lung cancer. The compositions

CC comprise one or more lung tumour polypeptides, immunogenic portions

CC thereof, polynucleotides that encode such polypeptides, antigen presenting

CC cells that express such polypeptides, and T cells that are specific for

CC cells expressing such polypeptides. The novel compositions have

CC cytostatic and immunostimulant activity. The lung tumour antigens can be

CC used in the creation of a vaccine. The polynucleotides that encode the

CC lung tumour polypeptides can be used in gene therapy to help in the

CC treatment of lung tumours. This sequence represents a human lung tumour

CC clone polypeptide of the invention. This sequence was not shown in the

CC specification. It has been taken from a World Intellectual Property

CC Organization CD ROM supplied with the specification.

XX

XX Sequence 235 AA;

SO

Query Match 100.0%; Score 1306; DB 7; Length 235;

Best/Local Similarity 100.0%; Pred. No. 4,5e-114;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLTLLPTBALGDAOBPGNMNEICLPLDVCRCALRLRYRDRYDTS 60

DB 1 MDPARPLGSLTLLPTBALGDAOBPGNMNEICLPLDVCRCALRLRYRDRYDTS 60

QY 61 CRQFLYGGEGNANNFYWEACDCAWRLEKVPKVCGLQVSVDDQEGSTKTFPILSSM 120

DB 61 CRQFLYGGEGNANNFYWEACDCAWRLEKVPKVCGLQVSVDDQEGSTKTFPILSSM 120

QY 121 TCSEKPSGGGCHRRRIENRFPDEATCMGFCAPKKIPSCFCSPKDBGLCSANVTYRNPXY 180

DB 121 TCSEKPSGGGCHRRRIENRFPDEATCMGFCAPKKIPSCFCSPKDBGLCSANVTYRNPXY 180

QY 181 RTCDATYTCGGGNDNNFVSRBDCKRACAKALKKKKMKPLRFPASIRIRKRRKQF 235

DB 181 RTCDATYTCGGGNDNNFVSRBDCKRACAKALKKKKMKPLRFPASIRIRKRRKQF 235

RESULT 11

ID ADI62727 standard; protein; 235 AA.

AC ADI62727;

XX

XX

XX 08-SEP-2005 (revised)

DT 22-APR-2004 (first entry)

DE

XX Human apoptosis-associated protein SEQ ID 170.

DE

XX apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;

KW antiinflammatory; antiarthritic; dermatological; antiparkinsonian;

KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;

KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;

KW autoimmune disease; degenerative disease; viral infection; leukaemia;

KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;

KW lupus; hepatitis; influenza viruses; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;

KW alcoholic liver disease; human.

XX

XX Homo sapiens.

OS

XX WO2003058021-A2.

PN

XX 17-JUL-2003.

PD

XX 13-JAN-2003; 2003WO-EP000270.

PF

XX 11-JAN-2002; 2002DE-01000856.

PR

XX

XX (XANT-) XANTOS BIOMEDICINE AG.

PA

XX

XX Koenig-Hoffman K, Kazinski M, Schaefer R, Keeper B;

PI WPI; 2003-542134/51.

XX

XX N-PSDB; AEA79039.

DR

XX

XX New nucleic acids involved in apoptosis, useful for diagnosis and

PT treatment of e.g. tumors and degenerative disease, also related proteins,

PT antibodies and modulators.

XX

XX Claim 1a; SEQ ID NO 170; 517bp; German.

PS

XX This invention describes novel nucleic acid molecules that are associated

XX with apoptosis and encode a polypeptide and are derived from a normalised

CC gene library (embryonic or liver) or clone collections, and the extent of

CC apoptosis measured by cell death detection assay or the CPG assay

CC (measuring loss of membrane integrity). The products of the invention

CC have cytostatic, neuroprotective, immunosuppressive, antiinflammatory,

CC antiarthritic, dermatological, immunosuppressive, hepatotropic, virucide,

CC nootropic, anticonvulsant, antiparkinsonian, vasotropic,

CC cerebroprotective and antialcoholic activity and can be used for gene

CC therapy. The polynucleotides also related vectors, hosts (or their

CC extracts), encoded polypeptide (or their receptors) and/or agents that

CC inhibit their activity (including antisense sequences) are used for

CC treatment or prevention of tumours, autoimmune or degenerative diseases

CC and viral infections, specifically leukaemia, carcinoma, sarcoma,

CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection

CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or

CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver

CC disease. Detection of the polynucleotides and derived polypeptides can

CC also be used for diagnosis of these diseases. This sequence represents an

CC apoptosis-associated protein described in the invention.

CC

CC Revised record issued on 08-SEP-2005 : Revision to cross-reference field

XX

XX Sequence 235 AA;

SO



Query Match 100.0%; Score 1306; DB 7; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGSLILLFLTEALGDAOEPGNNAICLLPLDYGPCRALLRYYDRYTQS 60  
Db 1 MDPAPPLGSLILLFLTEALGDAOEPGNNAICLLPLDYGPCRALLRYYDRYTQS 60

QY 61 CRQFLYGGCGGNANFTTWEACDCAWRIEKVPYCVLQVSVDDQCGSTEXKFFNLSSM 120  
Db 61 CRQFLYGGCGGNANFTTWEACDCAWRIEKVPYCVLQVSVDDQCGSTEXKFFNLSSM 120

QY 121 TCEKFFSGGCHRRRIENRFPDEATCMGFCAPKILPSFCYSPKDEGLCSANVTYYENPRY 180  
Db 121 TCEKFFSGGCHRRRIENRFPDEATCMGFCAPKILPSFCYSPKDEGLCSANVTYYENPRY 180

QY 181 RTCDAFYTYGCGGNDNNFVSRDCKRACAKALKKKKKMPKLRFASRIKIRKKQF 235  
Db 181 RTCDAFYTYGCGGNDNNFVSRDCKRACAKALKKKKKMPKLRFASRIKIRKKQF 235

RESULT 12  
ADN38706 standard; protein; 235 AA.

AC ADN38706;  
XX 17-JUN-2004 (first entry)  
XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:24.  
XX

Human; differential expression; cancer; angiogenic disorder;  
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
inflammatory disease; autoimmune disease;  
retinal neovascularisation syndrome; scarring; uterine fibroid;  
detection; diagnosis; prognosis; drug screening; drug targeting;  
wound healing; contraception; cytostatic; cardiac; immunomodulatory;  
vulnerable; gene therapy; vaccine.

OS Homo sapiens.  
XX  
XX WO2003042661-A2.  
XX  
XX 22-MAY-2003.  
XX  
XX 13-NOV-2002; 2002WO-US036810.  
XX  
XX 13-NOV-2001; 2001US-0350666P.  
XX 21-NOV-2001; 2001US-0332464P.  
XX 29-NOV-2001; 2001US-0334393P.  
XX 03-DEC-2001; 2001US-0335394P.  
XX 14-DEC-2001; 2001US-0340376P.  
XX 08-JAN-2002; 2002US-0347211P.  
XX 10-JAN-2002; 2002US-0347349P.  
XX 08-FEB-2002; 2002US-0355250P.  
XX 13-FEB-2002; 2002US-0356714P.  
XX 20-FEB-2002; 2002US-0359077P.  
XX 29-MAR-2002; 2002US-0368809P.  
XX 04-APR-2002; 2002US-0370110P.  
XX 12-APR-2002; 2002US-0372246P.  
XX 05-JUN-2002; 2002US-0386614P.  
XX 16-JUL-2002; 2002US-0396839P.  
XX 22-JUL-2002; 2002US-0397757P.  
XX 22-JUL-2002; 2002US-0397845P.  
XX 09-SEP-2002; 2002US-0409450P.  
XX  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA,  
XX Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;  
XX WPI; 2003-468649/44.  
XX  
XX N-PSDB; ADN38705.  
XX  
XX

XX Determining the presence or absence of a pathological cell in a patient,  
XX useful for diagnosing, prognosing or treating cancer, comprises detecting  
XX a nucleic acid in a biological sample.

PS Claim 12; SEQ ID NO 24; 1385bp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
XX whose expression is upregulated or downregulated in specific cancers or  
XX other diseases such as angiogenic or fibrotic disorders, and to methods  
XX of determining the presence or absence of a pathological cell in a  
XX patient by detecting a nucleic acid at least 80% identical to those of  
XX the invention or by detecting a polypeptide of the invention. The  
XX invention also relates to expression vectors and host cells comprising a  
XX nucleic acid of the invention; antibodies which specifically bind a  
XX polypeptide of the invention; use of such antibodies for drug targeting;  
XX and methods of screening for modulators of activity or expression of the  
XX polypeptides and nucleic acids. The nucleic acids, polypeptides, and  
XX antibodies and methods are useful for diagnosing, prognosing and treating  
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,  
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
XX neovascularisation syndromes, scarring and uterine fibroids. They may  
XX also be useful in wound healing and in contraception. The present  
XX sequence represents a polypeptide of the invention.

XX Sequence 235 AA;  
XX

Query Match 100.0%; Score 1306; DB 7; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAPPLGSLILLFLTEALGDAOEPGNNAICLLPLDYGPCRALLRYYDRYTQS 60  
Db 1 MDPAPPLGSLILLFLTEALGDAOEPGNNAICLLPLDYGPCRALLRYYDRYTQS 60

QY 61 CRQFLYGGCGGNANFTTWEACDCAWRIEKVPYCVLQVSVDDQCGSTEXKFFNLSSM 120  
Db 61 CRQFLYGGCGGNANFTTWEACDCAWRIEKVPYCVLQVSVDDQCGSTEXKFFNLSSM 120

QY 121 TCEKFFSGGCHRRRIENRFPDEATCMGFCAPKILPSFCYSPKDEGLCSANVTYYENPRY 180  
Db 121 TCEKFFSGGCHRRRIENRFPDEATCMGFCAPKILPSFCYSPKDEGLCSANVTYYENPRY 180

QY 181 RTCDAFYTYGCGGNDNNFVSRDCKRACAKALKKKKKMPKLRFASRIKIRKKQF 235  
Db 181 RTCDAFYTYGCGGNDNNFVSRDCKRACAKALKKKKKMPKLRFASRIKIRKKQF 235

RESULT 13  
ADE71603 standard; protein; 235 AA.

ID ADE71603;  
XX  
XX ADE71603;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Human lung tumour protein #9.  
XX  
XX Human lung tumour protein #9.  
XX  
XX human; lung tumour; cancer; lung cancer; vaccine.  
XX  
XX Homo sapiens.  
XX  
XX US2003125245-A1.  
XX  
XX 03-JUL-2003.  
XX  
XX 30-DEC-1999; 99US-00476300.  
XX  
XX 30-JUN-1999; 99US-00346492.  
XX 15-OCT-1999; 99US-00419356.  
XX 17-DEC-1999; 99US-00466867.  
XX  
XX (WANG/) WANG T.  
XX  
XX



PA (BANG/) BANGUR C S.  
XX  
XX Wang T, Bangur CS;  
XX  
XX WPI; 2004-059187/06.  
DR N-PSDB; ADB72120.  
XX  
XX Compositions and methods for the therapy and diagnosis of lung cancer  
PT based on the detection of a lung tumor polypeptide or immunogenic portion  
PT of this lung tumor protein.  
XX  
XX  
XX Claim 52; SEQ ID NO 332; 38pp; English.  
XX  
XX The invention relates to a polypeptide comprising at least an immunogenic  
CC portion of a lung tumor protein or variant. The invention is useful for  
CC inhibiting the development of a cancer, particularly lung cancer, in a  
CC patient by administering to a patient an effective amount of a  
CC polypeptide, an effective amount of the polynucleotide, an effective  
CC amount of an antibody or antigen-binding fragment an antigen-presenting  
CC cell that expresses a polypeptide where the antigen-presenting cell is a  
CC dendritic cell, a biological sample created by a method of the invention  
CC or an isolated T cell population prepared by a method of the invention.  
CC The pharmaceutical compositions and vaccines of the invention are also  
CC used for inhibiting the development of cancer. Methods are also provided  
CC for diagnosing cancer and also monitoring the progression of cancer.  
CC Current therapies of cancer are based on the combination of chemotherapy  
CC or surgery or radiation which prove to be inadequate in many patients.  
CC This invention provides effective vaccines and compositions which may be  
CC used in therapy. The compositions also provide early diagnostic  
CC procedures. The present sequence represents the amino acid sequence of a  
CC human lung tumour protein.  
XX  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 8; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGISTILLFLTEALGDAAOEPGNNARICLLPLDYGPCRALILRYRYRYS 60  
DB 1 MDPAPPLGISTILLFLTEALGDAAOEPGNNARICLLPLDYGPCRALILRYRYRYS 60  
QY 61 CROPFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDQCEGSTEKYPFNLSM 120  
DB 61 CROPFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDQCEGSTEKYPFNLSM 120  
QY 121 TCEKFPSSGCHRNRIENRPPDEATCMGFCAPKIKIPSPCYSPDEGLCSANTVRYFNPXY 180  
DB 121 TCEKFPSSGCHRNRIENRPPDEATCMGFCAPKIKIPSPCYSPDEGLCSANTVRYFNPXY 180  
QY 181 RTCDAPFTTGGCGDNNFVSRBDCRCRACAKALKKKKKMPKLRPASRIKIRKKOP 235  
DB 181 RTCDAPFTTGGCGDNNFVSRBDCRCRACAKALKKKKKMPKLRPASRIKIRKKOP 235  
RESULT 14  
ADL83255 standard; protein; 235 AA.  
ID ADL83255;  
AC ADL83255;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX Human PRO35972, SEQ ID 457.  
XX  
XX  
XX Immunosuppressive; Cytostatic; Antiarthritic; Antipneumatic; Antianemic;  
XX Antiallergic; Muscular; Neuroprotective; Nephroprotective; Antiinflammatory;  
XX Gene Therapy; PRO; B cell related disorder; cancer;  
XX Immune-mediated inflammatory disease; human.  
XX  
XX Homo sapiens.  
XX  
XX WO2004024097-A2.  
PN

XX  
XX 25-MAR-2004.  
XX  
XX 15-SEP-2003; 2003WO-US029097.  
XX  
XX 16-SEP-2002; 2002US-0411392P.  
XX  
XX (GERTH ) GENENTECH INC.  
XX  
XX Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
XX Wu TD;  
XX  
XX WPI; 2004-329389/30.  
DR N-PSDB; ADL83254.  
XX  
XX New PRO polypeptide, useful for diagnosing and treating a B cell related  
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
XX  
XX  
XX Claim 10; Fig 457; 695pp; English.  
XX  
XX The present invention relates to PRO proteins and their coding sequences.  
CC The PRO proteins are useful for diagnosing and treating a B cell related  
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide  
CC antigen unresponsiveness, selective IGA deficiency, selective IGM  
CC deficiency, selective deficiency of IGG subclasses, immunodeficiency with  
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic  
CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.  
XX  
XX  
XX Sequence 235 AA;  
SQ  
Query Match 100.0%; Score 1306; DB 8; Length 235;  
Best Local Similarity 100.0%; Pred. No. 4.5e-114;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAPPLGISTILLFLTEALGDAAOEPGNNARICLLPLDYGPCRALILRYRYRYS 60  
DB 1 MDPAPPLGISTILLFLTEALGDAAOEPGNNARICLLPLDYGPCRALILRYRYRYS 60  
QY 61 CROPFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDQCEGSTEKYPFNLSM 120  
DB 61 CROPFLYGGCEGNANFYTWBACDDACMRIBKYPKVCRLQVSDQCEGSTEKYPFNLSM 120  
QY 121 TCEKFPSSGCHRNRIENRPPDEATCMGFCAPKIKIPSPCYSPDEGLCSANTVRYFNPXY 180  
DB 121 TCEKFPSSGCHRNRIENRPPDEATCMGFCAPKIKIPSPCYSPDEGLCSANTVRYFNPXY 180  
QY 181 RTCDAPFTTGGCGDNNFVSRBDCRCRACAKALKKKKKMPKLRPASRIKIRKKOP 235  
DB 181 RTCDAPFTTGGCGDNNFVSRBDCRCRACAKALKKKKKMPKLRPASRIKIRKKOP 235  
RESULT 15  
ADL19770 standard; protein; 235 AA.  
ID ADL19770;  
AC ADL19770;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX Human lung cancer-related protein - SEQ ID 332.  
XX  
XX Lung tumour; cytostatic; lung cancer; human.  
XX  
XX

OS Homo sapiens.  
 XX US2003211510-A1.  
 XX 13-NOV-2003.  
 PD  
 XX 28-OCT-2002; 2002US-00283017.  
 PF  
 XX 30-JUN-1999; 99US-00346492.  
 PR 15-OCT-1999; 99US-00419356.  
 PR 17-DEC-1999; 99US-00466867.  
 PR 30-DEC-1999; 99US-00476300.  
 PR 06-MAR-2000; 2000US-00519642.  
 PR 22-MAR-2000; 2000US-00533077.  
 PR 10-APR-2000; 2000US-00546259.  
 PR 27-APR-2000; 2000US-00560406.  
 PR 05-JUN-2000; 2000US-00589184.  
 PR 11-JUL-2000; 2000US-00614124.  
 PR 29-AUG-2000; 2000US-00651563.  
 PR 08-SEP-2000; 2000US-00658824.  
 PR 26-SEP-2000; 2000US-00671325.  
 PR 06-OCT-2000; 2000US-00677419.  
 PR 30-OCT-2000; 2000US-00702705.  
 PR 13-DEC-2000; 2000US-00736457.  
 PR 03-MAY-2001; 2001US-00849626.  
 PR 10-JUL-2001; 2001US-00902941.  
 PR 29-OCT-2001; 2001US-00017754.  
 PR 28-MAR-2002; 2002US-00113872.

(CORI-) CORIXA CORP.

Henderson RA, Wang T, Watanabe Y, Kalos MD, Sleath PR,  
 Johnson JC, Retter MW, Durham M, Carter D, Fanger GR, Vedvick TS;  
 Bangur CS, McNabb A;

WPI: 2004-167010/16.  
 N-PSDB; ADI19502.

Novel polynucleotide encoding lung tumor polypeptides, useful for  
 diagnosing, preventing and treating cancer e.g. lung cancer.

Example 1; SEQ ID NO 332; 99pp; English.

The invention relates to a novel isolated polynucleotide comprising a  
 sequence chosen from any one of 40 lung tumour polypeptides or its  
 complements, fragments or degenerate variants. The method of the  
 invention has cytostatic applications and may be useful for detecting and  
 treating lung cancer in a patient, as well as for inhibiting the  
 development of lung cancer in a patient via incubating CD4+ and/or CD8+ T  
 cells isolated from a patient with at least one component chosen from a  
 polypeptide, polynucleotide or antigen presenting cell (APC) of the  
 invention and administering an effective amount of the proliferated T  
 cells to the patient. The current sequence is that of the human lung  
 cancer-related protein of the invention. The current sequence is not  
 shown in the specification per se but is available on the USPTO web-site  
 http://seqdata.uspto.gov/sequence.html?docid=20030211510.

Sequence 235 AA;

Query Match 100.0%; Score 1306; DB 9; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-114; Indels 0; Gaps 0;  
 Matches 235; Conservative 0; Mismatches 0;

QY 1 MDPARPLGISILLFLTEALGDAAEPTGNNAEICLPLDYGPCRALLIRYYDRTQS 60  
 DB 1 MDPARPLGISILLFLTEALGDAAEPTGNNAEICLPLDYGPCRALLIRYYDRTQS 60  
 QY 61 CRQFLYGGCEGNANFYTWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
 DB 61 CRQFLYGGCEGNANFYTWEACDCAWRIEKVPKVCRLQVSVDDQCEGSTERYFPNLSSM 120  
 QY 121 TCEKFPSCGCHRNRIENRPDEATCMGFCAPKLIPSFCTSPRDEGLCSANVTTRYFNPRY 180  
 DB 121 TCEKFPSCGCHRNRIENRPDEATCMGFCAPKLIPSFCTSPRDEGLCSANVTTRYFNPRY 180

Db 121 TCEKFPSCGCHRNRIENRPDEATCMGFCAPKLIPSFCTSPRDEGLCSANVTTRYFNPRY 180  
 QY 181 RTCDAFYTTGGGNDNNFVSRDECKRACAKLKKKKKPKLRFASRIKIRKKQF 235  
 Db 181 RTCDAFYTTGGGNDNNFVSRDECKRACAKLKKKKKPKLRFASRIKIRKKQF 235

Search completed: March 9, 2006, 19:52:52  
 Job time : 192 secs

Db 1185 CGGCAACAACCTTCACAGCGCGGAGAGCTGCGAGGATGCTGCTGC 1227

RESULT 5  
US-10-821-234-688

Sequence 688, Application US/10821234  
Publication No. US2005025511A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmeni, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

PRIOR FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pc\_SBO\_genes Version 1.0

SEQ ID NO 688

LENGTH: 915

TYPE: DNA

ORGANISM: Homo sapiens

US-10-821-234-688

Query Match 6.0%; Score 59; DB 8; Length 915;  
Best Local Similarity 52.7%; Pred. No. 0.0097;  
Matches 128; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 500 TCCATCATTTTCTCAGTCAAGTCAAAAGATGAGGAGCTGCTGCGCAATGTAAGTCTGCTA 559

Db 639 TCCCTCAAGTCTCTCACTCCAGCAGACAGAGATTTGTCTGTCATGATGAGAACAGATT 698

QY 560 TTATTTTATCCAGATACAGAACCTGTGATCTTCACTTACTGCTGTGAGGAA 619

Db 699 CTACTACATTCAGTCATGGAATGCGCCCATTTAGTACATGATGATGAGGAGAA 758

QY 630 TGACATTAACCTTTGTAGGAGGAGATGCGAACGTGATGCAAAAGCTTTGAAAA 679

Db 759 TGAAACAATTTTACTCTCCAAACAGAAATGTCGAGGGCATGTAAAAAGGTTTCATCCA 818

QY 680 GAAAAGAGATGCCAAGCTTGGCTTGGATGCAATCCGAAATTCGGAGAGCA 739

Db 819 AAGATATCAAAAGAGGCTTATTTAAACAAAAGAAAAAGAGAGAGCTGA 878

QY 740 ATT 742

Db 879 AAT 881

RESULT 6  
US-11-000-463-214

Sequence 214, Application US/11000463  
Publication No. US20050266423A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Chen, Rui-hong

APPLICANT: Qian, Xiaohong B.

APPLICANT: Wang, Zhiwei

APPLICANT: Wehrman, Tom

APPLICANT: Zhou, Jie

APPLICANT: Cao, Yi-Cheng

APPLICANT: Drmanac, Radjoje T.

TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides

FILE REFERENCE: 785CIPACN

CURRENT APPLICATION NUMBER: US/11/000,463

PRIOR FILING DATE: 2004-11-29

PRIOR APPLICATION NUMBER: 10/291,265

PRIOR FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: PCT/US01/02623

PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 09/922,279

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-25

PRIOR APPLICATION NUMBER: 09/617,746

PRIOR FILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 09/631,451

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 09/633,870

NUMBER OF SEQ ID NOS: 944

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 214

LENGTH: 1280

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (103)..(1158)

US-11-000-463-214

Query Match 5.8%; Score 56.8; DB 12; Length 1280;  
Best Local Similarity 59.1%; Pred. No. 0.0035;  
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 135 GCGAGATCTGTCTCTCCCTTACGATCAAGACCTTCGCGGCTTCTCTCGTTAC 194

Db 952 GTGGGCGCTTCATCTCCATGATGTCGGGGCCCTTCGAGCTTATCGATCTGCG 1011

QY 195 TACTACGACAGTACAGCAGAGCTGCGCCAGTTCTGTACGGGGGCTGCGAGGCAAC 254

Db 1012 GCATTGATGCTGTCAAGGAGAGTGCCTCTTCCCTACGGGGGCTGCGAGGCAAC 1071

QY 255 GCCAACAATTTCTACACCTGAGAGCTTGCAGACATGCTTCTG 298

Db 1072 GGAACAAGTCTTACTCAGAGAAGAGTGCAGAGATGACTCGGG 1115

RESULT 7  
US-11-177-506-2

Sequence 2, Application US/11177506  
Publication No. US20060029956A1

GENERAL INFORMATION:

APPLICANT: Beyer, Wayne F.

APPLICANT: Venetta, Thomas M.

APPLICANT: Groelke, John W.

APPLICANT: Blasius, Rainer H.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE

FILE REFERENCE: 46143/294851

CURRENT APPLICATION NUMBER: US/11/177,506

PRIOR FILING DATE: 2005-07-08

PRIOR APPLICATION NUMBER: 60/586,856

PRIOR FILING DATE: 2004-07-09

NUMBER OF SEQ ID NOS: 52

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1413

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (227)...(1285)

US-11-177-506-2

Query Match 5.8%; Score 56.8; DB 9; Length 1413;  
Best Local Similarity 59.1%; Pred. No. 0.0036;  
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 135 GCGAGATCTGTCTCTCCCTTACGATCAAGACCTTCGCGGCTTCTCTCGTTAC 194

Db 1076 GTGGGGGCTGCATCTCCCATATGTCGGGGCCCTGCCAGCCTTATCCAGCTCTGG 1135  
Qy 195 TACTACGACAGGTACACGACAGCTCCCGCAGTTCTCTGTACGCGGGCTGCCAGGGCAAC 254  
Db 1136 GCATTGATGCTGTACAGGGGGAAGTGCCTCTTCCCTTACGGGGGCTGCCAGGGCAAC 1195  
Qy 255 GCCAACAATTCTTACACCTCGGAGGGCTTCCGACAGTCTTGTG 298  
Db 1196 GGGAACAAGTTCTACTCAGAGAAGAGTGCAGAGTACTCGCG 1239

## RESULT 8

US-11-000-463-686  
; Sequence 686, Application US/11000463  
; Publication No. US20050266423A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Qian, Xiaohong B.  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Zhang, Jie  
; APPLICANT: Zhou, Ping  
; APPLICANT: Cao, Yi-Cheng  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
; FILE REFERENCE: 785CIPACN  
; CURRENT APPLICATION NUMBER: US/11/000,463  
; PRIOR FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/291,265  
; PRIOR FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/02623  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 09/922,279  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 686  
; LENGTH: 1464  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-000-463-686

Query Match 5.8%; Score 56.8; DB 12; Length 1464;  
Best Local Similarity 59.1%; Pred. No. 0.0036;  
Matches 97; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
Qy 135 GCGAGATCTGTCTCTGCGCCCTAGCTACGAGACCCCTCGGGCCCTTCTCCGTTAC 194  
Db 1137 GTGGGGGCTGCAATCTCCCATATGTCGGGGCCCTTCCAGCCTTATCAGCTCTGG 1196  
Qy 195 TACTACGACAGGTACACGACAGCTCCCGCAGTTCTGTACGGGGGCTGCCAGGGCAAC 254  
Db 1197 GCATTGATGCTGTACAGGGGGAAGTGCCTCTTCCCTTACGGGGGCTGCCAGGGCAAC 1256  
Qy 255 GCCAACAATTCTTACACCTCGGAGGGCTTCCGACAGTCTTGTG 298  
Db 1257 GGGAACAAGTTCTACTCAGAGAAGAGTGCAGAGTACTCGCG 1300

RESULT 9  
US-11-128-061-869  
; Sequence 869, Application US/11128061

; Publication No. US20060003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; PRIOR FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 869  
; LENGTH: 1234  
; TYPE: DNA  
; ORGANISM: Mesocricetus auratus  
; FEATURES:  
; NAME/KEY: misc\_feature  
; LOCATION: (876)..(891)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-128-061-869

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
Qy 119 GCCAACAAGAAATACCGGAGATCTGTCTGCGCCCTAGACTACGAGACCTCGCGGCG 178  
Db 915 GCACACGCGCGGACCGTAGGCGGCTGCACTCTCCCATATGTCAGAGTCCCTCGCGTGC 974  
Qy 179 CCTACTCTCCGTTACTACTACGACAGGTACACGAGCTGCCGCGCAGTTCTGTACGG 238  
Db 975 CTAGCTGAGCTGTGGCATTCGATGCAGACAGGAAGAAATGCGTCCAGTTCAATTATGG 1034  
Qy 239 GGGCTGCGAGGGCAACGCCAACAATTTCTACCTGTGGAGGCTTCCAGCA 289  
Db 1035 CGGCTGCAGGAAGCAACGCAAGTTCTACTCCGAGAGGAGTGCAGGA 1085

RESULT 10  
US-11-128-061-4511  
; Sequence 4511, Application US/11128061  
; Publication No. US2006003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; PRIOR FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4511  
; LENGTH: 1234  
; TYPE: DNA  
; ORGANISM: Mesocricetus auratus  
; FEATURES:

NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-061-4511

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCTTACGAGACCTTGGCGGC 178  
DB 915 GCAAGCGCGGACCGTACGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGAGGAGCGCGCGCGAGTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACAGCAGAGGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCAACGCGCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGCGCAATTTCTACTCCGAGAGAGTGCAGGA 1085

## RESULT 11

US-11-128-049-869  
Sequence 869, Application US/11128049  
Publication No. US20060010513A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
TITLE OF INVENTION: MAKING AND USING SAME  
FILE REFERENCE: 01997.027700  
CURRENT APPLICATION NUMBER: US/11/128,049  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 869  
LENGTH: 1234  
TYPE: DNA  
ORGANISM: Mesocricetus auratus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-049-869

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCTTACGAGACCTTGGCGGC 178  
DB 915 GCAAGCGCGGACCGTACGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGAGGAGCGCGCGAGTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACAGCAGAGGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCAACGCGCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGCGCAATTTCTACTCCGAGAGAGTGCAGGA 1085

RESULT 12  
US-11-128-049-4511

Sequence 4511, Application US/11128049  
Publication No. US20060010513A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
TITLE OF INVENTION: MAKING AND USING SAME  
FILE REFERENCE: 01997.027700  
CURRENT APPLICATION NUMBER: US/11/128,049  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 4511  
LENGTH: 1234  
TYPE: DNA  
ORGANISM: Mesocricetus auratus  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8761..(891)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-128-049-4511

Query Match 5.4%; Score 52.6; DB 12; Length 1234;  
Best Local Similarity 56.7%; Pred. No. 0.031;  
Matches 97; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 119 GCCAAGGAAATTAACGGGAGATCTGCTCTGCTTACGAGACCTTGGCGGC 178  
DB 915 GCAAGCGCGGACCGTACGCGGCTGCGAGTCTCCCAATAGCCAAAGGCTCCGCGCGC 974  
QY 179 CCTACTTCCGTTACTACTAGAGGTACAGAGGAGCGCGCGAGTTCTGTACGG 238  
DB 975 CTACCTCAGCTCTGGGCAATTCGATGACAGCAGAGGAAATGCTCCAGTTCAATTATGG 1034  
QY 239 GGGCTGCGAGGCAACGCGCAATTTCTACACCTGGAGGCTTCCGACGA 289  
DB 1035 CGGCTGCAAGGCAACGCGCAATTTCTACTCCGAGAGAGTGCAGGA 1085

## RESULT 13

US-11-128-061-6860  
Sequence 6860, Application US/11128061  
Publication No. US2006003958A1  
GENERAL INFORMATION:  
APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane B.  
APPLICANT: Sinacore, Martin S.  
APPLICANT: Leonard, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
FILE REFERENCE: 01997.027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 6860  
LENGTH: 600  
TYPE: DNA  
ORGANISM: Cricetus griseus

US-11-128-061-6860

Query Match 5.3%; Score 52; DB 12; Length 600;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 225 CATTTTGGCCAAATGAAGGTAGATGATGACCCGTGCMAACCATGATGAGAGTTATTTT 284  
 |||||  
 QY 565 TTAATCCAAATACAGAACTGTGATCTTTCACTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 285 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 344  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCAAAGCTGCATGTGCMAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 345 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 404  
 |||||

RESULT 14

US-11-128-049-6860

Sequence 6860, Application US/11128049  
 Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.  
 APPLICANT: Charlebois, Timothy S.  
 APPLICANT: Mounts, William W.  
 APPLICANT: Hann, Louane E.  
 APPLICANT: Sinacore, Martin S.  
 APPLICANT: Leonard, Mark W.  
 APPLICANT: Brown, Eugene L.  
 APPLICANT: Miller, Christopher P.  
 TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
 FILE REFERENCE: 01997.027700  
 CURRENT APPLICATION NUMBER: US/11/128,049  
 PRIOR FILING DATE: 2005-05-11  
 PRIOR APPLICATION NUMBER: US 60/570,425  
 NUMBER OF SEQ ID NOS: 7285  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 6860  
 LENGTH: 600  
 TYPE: DNA  
 ORGANISM: Cricetus griseus  
 US-11-128-049-6860

Query Match 5.3%; Score 52; DB 12; Length 600;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 225 CATTTTGGCCAAATGAAGGTAGATGATGACCCGTGCMAACCATGATGAGAGTTATTTT 284  
 |||||  
 QY 565 TTAATCCAAATACAGAACTGTGATCTTTCACTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 285 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 344  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCAAAGCTGCATGTGCMAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 345 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 404  
 |||||

RESULT 15

US-11-128-061-3218

Sequence 3218, Application US/11128061  
 Publication No. US20060003958A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.  
 APPLICANT: Charlebois, Timothy S.  
 APPLICANT: Mounts, William W.  
 APPLICANT: Hann, Louane E.

APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.

APPLICANT: Brown, Eugene L.

APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS

FILE REFERENCE: 01997.027701

CURRENT APPLICATION NUMBER: US/11/128,061

PRIOR FILING DATE: 2005-05-11

PRIOR APPLICATION NUMBER: US 60/570,425

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: PatentIn version 3.3

SEQ ID NO 3218

LENGTH: 650

TYPE: DNA

ORGANISM: Cricetus griseus

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(21)

OTHER INFORMATION: n is a, c, g, or t

US-11-128-061-3218

Query Match 5.3%; Score 52; DB 12; Length 650;  
 Best Local Similarity 55.6%; Pred. No. 0.033;  
 Matches 100; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 505 CATTTTGCTACAGTCCAAAAGATGAGGAGCTGTGCTCTGCCAATGTGACTCGCTATTATT 564  
 |||||  
 DB 275 CATTTTGGCCAAATGAAGGTAGATGATGACCCGTGCMAACCATGATGAGAGTTATTTT 334  
 |||||  
 QY 565 TTAATCCAAATACAGAACTGTGATCTTTCACTATCTGCTGTGAGGGAATGACA 624  
 |||||  
 DB 335 TCAATATTTTACTTACCAATGTGAAGATTATATATGGGGATGCAGAGAAACGAAA 394  
 |||||  
 QY 625 ATAACTTTGTAGAGGAGATGTCAAAGCTGCATGTGCMAAAGCTTTGAAAAAGAAA 684  
 |||||  
 DB 395 ATCGATTTGAAACCTGGAGAGATGTAAAGAGACATGCATCAGAGGTTATTAAGAAAGA 454  
 |||||

Search completed: March 11, 2006, 06:32:19  
 Job time : 438 secs